

SEQUENCE LISTING

<110> O'Donnell, Michael E.
Yuzhakov, Alexander
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Jeruzalmi, David
Bruck, Irina
Kuriyan, John

<120> ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
USE THEREOF

<130> 22221/1030

<140> 09/716,964

<141> 2000-11-21

<150> 60/143,202

<151> 1997-04-08

<150> 08/823,407

<151> 1997-04-08

<150> 09/057,416

<151> 1998-04-08

<160> 212

<170> PatentIn Ver. 2.1

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<211> 2007

<212> DNA

<213> Thermus thermophilus

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<211> 529

<212> PRT

<213> *Thermus thermophilus*

<400> 2

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15

Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu

20

25

30

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly

35

40

45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly

50

55

60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg

65

70

75

80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser

85

90

95

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
100 105 110
Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
115 120 125
Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
130 135 140
His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
145 150 155 160
Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
165 170 175
Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
180 185 190
Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
195 200 205
Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
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Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
225 230 235 240
Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
245 250 255
Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
260 265 270
Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
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Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
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Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
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Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
325 330 335
Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
340 345 350

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
 355 360 365

Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
 370 375 380

Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
 385 390 395 400

Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
 405 410 415

Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
 420 425 430

Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
 435 440 445

Gly Glu Lys Lys Ser Leu Ser Pro Arg Pro Arg Pro Ala Pro Pro Pro
 450 455 460

Glu Ala Pro Ala Pro Pro Gly Pro Pro Glu Glu Glu Val Glu Ala Glu
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Glu Ala Ala Glu Glu Ala Pro Glu Glu Ala Leu Arg Arg Val Val Arg
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Leu Leu Gly Gly Arg Val Leu Trp Val Arg Arg Pro Arg Thr Arg Glu
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 <212> DNA
 <213> Thermus thermophilus

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<211> 464

<212> PRT

<213> *Thermus thermophilus*

<400> 4

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15

Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu

20

25

30

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly

35

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45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly

50

55

60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg

65

70

75

80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser

85

90

95

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
100 105 110
Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
115 120 125
Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
130 135 140
His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
145 150 155 160
Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
165 170 175
Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
180 185 190
Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
195 200 205
Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
210 215 220
Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
225 230 235 240
Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
245 250 255
Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
260 265 270
Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
275 280 285
Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
290 295 300
Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
305 310 315 320
Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
325 330 335
Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
340 345 350

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
 355 360 365
 Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
 370 375 380
 Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
 385 390 395 400
 Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
 405 410 415
 Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
 420 425 430
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 Gly Glu Lys Lys Lys Pro Glu Pro Lys Ala Pro Pro Gly Pro Thr Ser
 450 455 460

<210> 5
 <211> 454
 <212> PRT
 <213> Thermus thermophilus

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 20 25 30
 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
 35 40 45
 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 50 55 60
 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65 70 75 80
 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser

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Ser	Ala	Pro	Arg	Lys	Val	Phe	Ile	Leu	Asp	Glu	Ala	His	Met	Leu	Ser
			115					120					125		
Lys	Ser	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	Glu	Pro	Pro	Pro
			130					135					140		
His	Val	Leu	Phe	Val	Phe	Ala	Thr	Thr	Glu	Pro	Glu	Arg	Met	Pro	Pro
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Thr	Ile	Leu	Ser	Arg	Thr	Gln	His	Phe	Arg	Phe	Arg	Arg	Leu	Thr	Glu
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Glu	Glu	Ile	Ala	Phe	Lys	Leu	Arg	Arg	Ile	Leu	Glu	Ala	Val	Gly	Arg
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			210					215				220			
Gly	Pro	Leu	Thr	Arg	Lys	Glu	Val	Glu	Arg	Ala	Leu	Gly	Ser	Pro	Pro
225					230					235					240
Gly	Thr	Gly	Val	Ala	Glu	Ile	Ala	Ala	Ser	Leu	Ala	Arg	Gly	Lys	Thr
				245					250						255
Ala	Glu	Ala	Leu	Gly	Leu	Ala	Arg	Arg	Leu	Tyr	Gly	Glu	Gly	Tyr	Ala
			260					265					270		
Pro	Arg	Ser	Leu	Val	Ser	Gly	Leu	Leu	Glu	Val	Phe	Arg	Glu	Gly	Leu
			275					280					285		
Tyr	Ala	Ala	Phe	Gly	Leu	Ala	Gly	Thr	Pro	Leu	Pro	Ala	Pro	Pro	Gln
			290					295				300			
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Ala	Arg	Arg	Ser	Asp	Ala	Leu	Ser	Leu	Glu	Val	Ala	Leu	Leu	Glu	Ala
				325					330					335	
Gly	Arg	Ala	Leu	Ala	Ala	Glu	Ala	Leu	Pro	Gln	Pro	Thr	Gly	Ala	Pro

340	345	350
Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro		
355	360	365
Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe		
370	375	380
Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg		
385	390	400
Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys		
405	410	415
Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro		
420	425	430
Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu		
435	440	445
Gly Glu Lys Lys Lys Ala		
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<210> 6
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 6
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32

<210> 7
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 7
 His Ala Tyr Leu Phe Ser Gly Thr
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<210> 8
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 8
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<210> 9
 <211> 9
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: peptide

 <400> 9
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<210> 10
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

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<210> 11
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 11
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<210> 12
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 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 12
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 <210> 13
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 13
 gcgcgaattc gcgcttcggg aggtggg 27

 <210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 14
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 <210> 15
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 15
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<210> 16
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 16
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31

<210> 17
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<213> Artificial Sequence

<220>
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<222> (2)
<223> X is any aa at position 2

<220>
<221> PEPTIDE
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<223> X is any aa at position 3

<220>
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<223> X is any aa at position 5

<400> 17
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1 5

<210> 18
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 18

Lys Pro Asp Pro Lys Ala Pro Pro Gly Pro Thr Ser
1 5 10

<210> 19

<211> 180

<212> PRT

<213> Escherichia coli

<400> 19

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala
1 5 10 15

Asp Val Val Gly Gln Glu His Val Leu Thr Ala Leu Ala Asn Gly Leu
20 25 30

Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
50 55 60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
65 70 75 80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
100 105 110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Ala Leu Asp Val
180

<210> 20
 <211> 180
 <212> PRT
 <213> Bacillus subtilis

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 35 40 45
 Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
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 Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys
 65 70 75 80
 Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala
 85 90 95
 Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys
 100 105 110
 Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val
 115 120 125
 His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
 130 135 140
 Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His
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 165 170 175
 Arg Ile Thr Ser
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<210> 21
 <211> 294
 <212> PRT

<213> Escherichia coli

<400> 21

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Ser	Leu	Gly	Arg	Ile	His	His	Ala	Tyr	Leu	Phe	Ser	Gly	Thr	Arg	Gly	
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Ser	Arg	Thr	Lys	Val	Glu	Asp	Thr	Arg	Asp	Leu	Leu	Asp	Asn	Val	Gln	
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Tyr	Ala	Pro	Ala	Arg	Gly	Arg	Phe	Lys	Val	Tyr	Leu	Ile	Asp	Glu	Val	
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Glu	Pro	Pro	Glu	His	Val	Lys	Phe	Leu	Leu	Ala	Thr	Thr	Asp	Pro	Gln	
145				150						155					160	
Lys	Leu	Pro	Val	Thr	Ile	Leu	Ser	Arg	Cys	Leu	Gln	Phe	His	Leu	Lys	
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Ala	Leu	Asp	Val	Glu	Gln	Ile	Arg	His	Gln	Leu	Glu	His	Ile	Leu	Asn	
		180						185					190			
Glu	Glu	His	Ile	Ala	His	Glu	Pro	Arg	Ala	Leu	Gln	Leu	Leu	Ala	Arg	
	195						200					205				
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	210					215					220					
Ile	Ala	Ser	Gly	Asp	Gly	Gln	Val	Ser	Thr	Gln	Ala	Val	Ser	Ala	Met	
225					230					235					240	

Leu Gly Thr Leu Asp Asp Asp Gln Ala Leu Ser Leu Val Glu Ala Met
245 250 255

Val Glu Ala Asn Gly Glu Arg Val Met Ala Leu Ile Asn Glu Ala Ala
260 265 270

Ala Arg Gly Ile Glu Trp Glu Ala Leu Leu Val Glu Met Leu Gly Leu
275 280 285

Leu His Arg Ile Ala Met
290

<210> 22

<211> 294

<212> PRT

<213> Haemophilus influenzae

<400> 22

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Lys Thr Phe Ala
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Asp Val Val Gly Gln Glu His Ile Ile Thr Ala Leu Ala Asn Gly Leu
20 25 30

Lys Asp Asn Arg Leu His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Phe Ala Lys Gly Leu Asn Cys
50 55 60

Val His Gly Val Thr Ala Thr Pro Cys Gly Glu Cys Glu Asn Cys Lys
65 70 75 80

Ala Ile Glu Gln Gly Asn Phe Ile Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Glu Leu Leu Asp Asn Val Gln
100 105 110

Tyr Lys Pro Val Val Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu Tyr Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Ala Leu Asp Glu Thr Gln Ile Ser Gln His Leu Ala His Ile Leu Thr
180 185 190

Gln Glu Asn Ile Pro Phe Glu Asp Pro Ala Leu Val Lys Leu Ala Lys
195 200 205

Ala Ala Gln Gly Ser Ile Arg Asp Ser Leu Ser Leu Thr Asp Gln Ala
210 215 220

Ile Ala Met Gly Asp Arg Gln Val Thr Asn Asn Val Val Ser Asn Met
225 230 235 240

Leu Gly Leu Leu Asp Asp Asn Tyr Ser Val Asp Ile Leu Tyr Ala Leu
245 250 255

His Gln Gly Asn Gly Glu Leu Leu Met Arg Thr Leu Gln Arg Val Ala
260 265 270

Asp Ala Ala Gly Asp Trp Asp Lys Leu Leu Gly Glu Cys Ala Glu Lys
275 280 285

Leu His Gln Ile Ala Leu
290

<210> 23
<211> 294
<212> PRT
<213> Bacillus subtilis

<400> 23
Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu
1 5 10 15

Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu
20 25 30

Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
35 40 45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
50 55 60

Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys

65		70		75		80
Gly Ile Thr Asn	Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala					
	85		90		95	
Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys						
	100		105		110	
Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val						
	115		120		125	
His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu						
	130		135		140	
Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His						
	145		150		155	160
Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys						
	165		170		175	
Arg Ile Thr Ser Gln Ala Ile Val Gly Arg Met Asn Lys Ile Val Asp						
	180		185		190	
Ala Glu Gln Leu Gln Val Glu Glu Gly Ser Leu Glu Ile Ile Ala Ser						
	195		200		205	
Ala Ala His Gly Gly Met Arg Asp Ala Leu Ser Leu Leu Asp Gln Ala						
	210		215		220	
Ile Ser Phe Ser Gly Asp Ile Leu Lys Val Glu Asp Ala Leu Leu Ile						
	225		230		235	240
Thr Gly Ala Val Ser Gln Leu Tyr Ile Gly Lys Leu Ala Lys Ser Leu						
	245		250		255	
His Asp Lys Asn Val Ser Asp Ala Leu Glu Thr Leu Asn Glu Leu Leu						
	260		265		270	
Gln Gln Gly Lys Asp Pro Ala Lys Leu Ile Glu Asp Met Ile Phe Tyr						
	275		280		285	
Phe Arg Asp Met Leu Leu						
	290					

<210> 24
 <211> 300
 <212> PRT

<213> Caulobacter crescentus

<400> 24

Asp Ala Tyr Thr Val Leu Ala Arg Lys Tyr Arg Pro Arg Thr Phe Glu
1 5 10 15

Asp Leu Ile Gly Gln Glu Ala Met Val Arg Thr Leu Ala Asn Ala Phe
20 25 30

Ser Thr Gly Arg Ile Ala His Ala Phe Met Leu Thr Gly Val Arg Gly
35 40 45

Val Gly Lys Thr Thr Thr Ala Arg Leu Leu Ala Arg Ala Leu Asn Tyr
50 55 60

Glu Thr Asp Thr Val Lys Gly Pro Ser Val Asp Leu Thr Thr Glu Gly
65 70 75 80

Tyr His Cys Arg Ser Ile Ile Glu Gly Arg His Met Asp Val Leu Glu
85 90 95

Leu Asp Ala Ala Ser Arg Thr Lys Val Asp Glu Met Arg Glu Leu Leu
100 105 110

Asp Gly Val Arg Tyr Ala Pro Val Glu Ala Arg Tyr Lys Val Tyr Ile
115 120 125

Ile Asp Glu Val His Met Leu Ser Thr Ala Ala Phe Asn Ala Leu Leu
130 135 140

Lys Thr Leu Glu Glu Pro Pro Pro His Ala Lys Phe Ile Phe Ala Thr
145 150 155 160

Thr Glu Ile Arg Lys Val Pro Val Thr Ile Leu Ser Arg Cys Gln Arg
165 170 175

Phe Asp Leu Arg Arg Val Glu Pro Asp Val Leu Val Lys His Phe Asp
180 185 190

Arg Ile Ser Ala Lys Glu Gly Ala Arg Ile Glu Met Asp Ala Leu Ala
195 200 205

Leu Ile Ala Arg Ala Ala Glu Gly Ser Val Arg Asp Gly Leu Ser Leu
210 215 220

Leu Asp Gln Ala Ile Val Gln Thr Glu Arg Gly Gln Thr Val Thr Ser
225 230 235 240

Thr Val Val Arg Asp Met Leu Gly Leu Ala Asp Arg Ser Gln Thr Ile
245 250 255

Ala Leu Tyr Glu His Val Met Ala Gly Lys Thr Lys Asp Ala Leu Glu
260 265 270

Gly Phe Arg Ala Leu Trp Gly Phe Gly Ala Asp Pro Ala Val Val Met
275 280 285

Leu Asp Val Leu Asp His Cys His Ala Ser Ala Val
290 295 300

<210> 25

<211> 260

<212> PRT

<213> Mycoplasma genitalium

<400> 25

Met His Gln Val Phe Tyr Gln Lys Tyr Arg Pro Ile Asn Phe Lys Gln
1 5 10 15

Thr Leu Gly Gln Glu Ser Ile Arg Lys Ile Leu Val Asn Ala Ile Asn
20 25 30

Arg Asp Lys Leu Pro Asn Gly Tyr Ile Phe Ser Gly Glu Arg Gly Thr
35 40 45

Gly Lys Thr Thr Phe Ala Lys Ile Ile Ala Lys Ala Ile Asn Cys Leu
50 55 60

Asn Trp Asp Gln Ile Asp Val Cys Asn Ser Cys Asp Val Cys Lys Ser
65 70 75 80

Ile Asn Thr Asn Ser Ala Ile Asp Ile Val Glu Ile Asp Ala Ala Ser
85 90 95

Lys Asn Gly Ile Asn Asp Ile Arg Glu Leu Val Glu Asn Val Phe Asn
100 105 110

His Pro Phe Thr Phe Lys Lys Lys Val Tyr Ile Leu Asp Glu Ala His
115 120 125

Met Leu Thr Thr Gln Ser Trp Gly Gly Leu Leu Lys Thr Leu Glu Glu
130 135 140

Ser Pro Pro Tyr Val Leu Phe Ile Phe Thr Thr Thr Glu Phe Asn Lys
145 150 155 160

Ile Pro Leu Thr Ile Leu Ser Arg Cys Gln Ser Phe Phe Phe Lys Lys
 165 170 175
 Ile Thr Ser Asp Leu Ile Leu Glu Arg Leu Asn Asp Ile Ala Lys Lys
 180 185 190
 Glu Lys Ile Lys Ile Glu Lys Asp Ala Leu Ile Lys Ile Ala Asp Leu
 195 200 205
 Ser Gln Gly Ser Leu Arg Asp Gly Leu Ser Leu Leu Asp Gln Leu Ala
 210 215 220
 Ile Ser Leu Ile Val Lys Lys Leu Val Leu Leu Met Leu Lys Lys His
 225 230 235 240
 Leu Ile Ser Leu Ile Glu Met Gln Asn Leu Leu Leu Leu Lys Gln Phe
 245 250 255
 Tyr Gln Glu Ile
 260

<210> 26
 <211> 289
 <212> PRT
 <213> *Thermus thermophilus*

<400> 26
 Val Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
 1 5 10 15
 Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
 20 25 30
 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
 35 40 45
 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 50 55 60
 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65 70 75 80
 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
 85 90 95
 Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu

100	105	110
Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser		
115	120	125
Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro		
130	135	140
His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro		
145	150	155
Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu		
165	170	175
Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg		
180	185	190
Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly		
195	200	205
Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu		
210	215	220
Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro		
225	230	235
Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr		
245	250	255
Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala		
260	265	270
Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu		
275	280	285
Tyr		

<210> 27

<211> 94

<212> DNA

<213> Thermus thermophilus

<400> 27

gccggaggga gaaaaaaaaa gccgagccca agggccccgcc cggccccacc ccgaagcgcc	60
cgcacccccg ggccccccga ggaggaggag aggc	94

<210> 28
<211> 11
<212> PRT
<213> Thermus thermophilus

<400> 28
Val Leu Glu Gly Glu Lys Lys Ser Leu Ser Pro
1 5 10

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> (6)
<223> N at position 6 is either G or C

<220>
<221> unsure
<222> (12)
<223> N at position 12 is either G or C

<220>
<221> unsure
<222> (21)
<223> N at position 21 is either G or C

<400> 29
cacgcntacc tnttctccgg nac 23

<210> 30
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure

<222> (7)
<223> N at position 7 is either G or C

<220>
<221> unsure
<222> (10)
<223> N at position 10 is either G or C

<220>
<221> unsure
<222> (19)
<223> N at position 19 is either G or C

<220>
<221> unsure
<222> (22)
<223> N at position 22 is either G or C

<400> 30
gtgctcnggn ggctcctcnt cngtc 25

<210> 31
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 31
gtgggatccg tggttctgga tctcgatgaa gaa 33

<210> 32
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 32
gtgggatcca cggsctstcs gagcagaag 29

<210> 33
<211> 34

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 33
 gcgggatacct caacgaggac ctctccatct tcaa 34

 <210> 34
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 34
 gcgggatacct tgtcgtcsag sgtsagsgcg tcgta 35

 <210> 35
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 35
 gggaaggacc agcgcgtact cccctgctc ctaggtgtg 39

 <210> 36
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 36
 gtgtggatcc ttcttcttsc ccatsgc 27

 <210> 37
 <211> 27

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 37
 caccgattcc agtggtgcct aggtgtg 27

 <210> 38
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 38
 caacacctgg tgttcagga gcctgtgctt 30

 <210> 39
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 39
 ccagaatcgt ctgctggtcg tag 23

 <210> 40
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 40
 agcaccctgg aggagcttc 19

 <210> 41
 <211> 19

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 41
catgtcgtac tgggtgtac

19

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> (7)
<223> N at position 7 is A, C, G, or T

<220>
<221> unsure
<222> (8)
<223> N at position 8 is A, C, G, or T

<220>
<221> unsure
<222> (13)
<223> N at position 13 is A, C, G, or T

<220>
<221> unsure
<222> (14)
<223> N at position 14 is A, C, G, or T

<400> 42
gtsgtsnns acnns gagac sacsggg

27

<210> 43
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> unsure

<222> (8)

<223> N at position 8 is A, C, G, or T

<220>

<221> unsure

<222> (9)

<223> N at position 9 is A, C, G, or T

<220>

<221> unsure

<222> (17)

<223> N at position 17 is A, C, G, or T

<220>

<221> unsure

<222> (18)

<223> N at position 18 is A, C, G, or T

<400> 43

gaasccsnng tcgaasnngg cgttgtg

27

<210> 44

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 44

cggggatcca cctcaatcac ctctgtg

27

<210> 45

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 45

cggggatccg ccaccttgcg gctccgggtg

30

<210> 46
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 46
gcgctctaga cgagttccca aagcgtgcgg t 31

<210> 47
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 47
cgcgctctaga tcacctgtat ccaga 25

<210> 48
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 48
gcggcgcata tgggtggtggt cctggacctg gag 33

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 49
cgcgctctaga tcacctgtat ccaga 25

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 50
gtsctsgttsa agacscactt

20

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 51
sagsagsgcg ttgaasgtgt g

21

<210> 52
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 52
ctcgttggtg aaagtttccg tg

22

<210> 53
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 53
ctcgttggtg aaagtttccg tg

22

<210> 54
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 54
tctggcaaca cgttctggag cacatcc

27

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 55
tgctggcgtt catcttcagg atg

23

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 56
catcctgaag atgaacgcca gca

23

<210> 57
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 57
aggttatcca caggggtcat gtgca

25

<210> 58
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 58
gtgtgtcata tgaacataac gggtcccaa 29

<210> 59
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 59
gcgcgaattc tcccttgtag aaggcttag 29

<210> 60
<211> 13
<212> PRT
<213> Thermus thermophilus

<400> 60
Arg Val Glu Leu Asp Tyr Asp Ala Leu Thr Leu Asp Asp
1 5 10

<210> 61
<211> 14
<212> PRT
<213> Thermus thermophilus

<400> 61
Phe Phe Ile Glu Ile Gln Asn His Gly Leu Ser Glu Gln Lys
1 5 10

<210> 62
<211> 8

<212> PRT
<213> Thermus thermophilus

<400> 62
Phe Phe Ile Glu Ile Gln Asn His
1 5

<210> 63
<211> 8
<212> PRT
<213> Thermus thermophilus

<400> 63
Tyr Asp Ala Leu Thr Leu Asp Asp
1 5

<210> 64
<211> 6
<212> PRT
<213> Thermus thermophilus

<400> 64
Ala Met Gly Lys Lys Lys
1 5

<210> 65
<211> 9
<212> PRT
<213> Thermus thermophilus

<400> 65
Phe Asn Lys Ser His Ser Ala Ala Tyr
1 5

<210> 66
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE

<222> (3)
<223> Xaa at position 3 is undefined

<220>
<221> PEPTIDE
<222> (5)
<223> Xaa at position 5 is undefined

<400> 66
Val Val Xaa Asp Xaa Glu Thr Thr Gly
1 5

<210> 67
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (4)
<223> Xaa at position 4 is undefined

<220>
<221> PEPTIDE
<222> (7)
<223> Xaa at position 7 is undefined

<400> 67
His Asn Ala Xaa Phe Asp Xaa Gly Phe
1 5

<210> 68
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (3)
<223> Xaa at position 3 is undefined

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<220>
<221> PEPTIDE
<222> (5)
<223> Xaa at position 5 is undefined

<400> 68
Val Val Xaa Asp Xaa Glu Thr Thr Gly
  1                      5

<210> 69
<211> 7
<212> PRT
<213> Thermus thermophilus

<400> 69
Val Leu Val Lys Thr His Leu
  1                      5

<210> 70
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  peptide

<400> 70
His Arg Ala Leu Tyr Asp
  1                      5

<210> 71
<211> 7
<212> PRT
<213> Thermus thermophilus

<400> 71
His Thr Phe Asn Ala Leu Leu
  1                      5

<210> 72
<211> 34
<212> PRT
<213> Escherichia coli

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<400> 72

Asp Arg Tyr Phe Leu Glu Leu Ile Arg Thr Gly Arg Pro Asp Glu Glu
1 5 10 15

Ser Tyr Leu His Ala Ala Val Glu Leu Ala Glu Ala Arg Gly Leu Pro
20 25 30

Val Val

<210> 73

<211> 34

<212> PRT

<213> *Vibrio cholerae*

<400> 73

Asp His Phe Tyr Leu Glu Leu Ile Arg Thr Gly Arg Ala Asp Glu Glu
1 5 10 15

Ser Tyr Leu His Phe Ala Leu Asp Val Ala Glu Gln Tyr Asp Leu Pro
20 25 30

Val Val

<210> 74

<211> 34

<212> PRT

<213> *Haemophilus influenzae*

<400> 74

Asp His Phe Tyr Leu Ala Leu Ser Arg Thr Gly Arg Pro Asn Glu Glu
1 5 10 15

Arg Tyr Ile Gln Ala Ala Leu Lys Leu Ala Glu Arg Cys Asp Leu Pro
20 25 30

Leu Val

<210> 75

<211> 34

<212> PRT

<213> *Rickettsia prowazekii*

<400> 75

Asp Arg Phe Tyr Phe Glu Ile Met Arg His Asp Leu Pro Glu Glu Gln
1 5 10 15

Phe Ile Glu Asn Ser Tyr Ile Gln Ile Ala Ser Glu Leu Ser Ile Pro
20 25 30

Ile Val

<210> 76

<211> 34

<212> PRT

<213> *Helicobacter pylori*

<400> 76

Asp Asp Phe Tyr Leu Glu Ile Met Arg His Gly Ile Leu Asp Gln Arg
1 5 10 15

Phe Ile Asp Glu Gln Val Ile Lys Met Ser Leu Glu Thr Gly Leu Lys
20 25 30

Ile Ile

<210> 77

<211> 34

<212> PRT

<213> *Synechocystis* sp.

<400> 77

Asp Asp Tyr Tyr Leu Glu Ile Gln Asp His Gly Ser Val Glu Asp Arg
1 5 10 15

Leu Val Asn Ile Asn Leu Val Lys Ile Ala Gln Glu Leu Asp Ile Lys
20 25 30

Ile Val

<210> 78

<211> 34

<212> PRT

<213> *Mycobacterium tuberculosis*

<400> 78

Asp Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Thr Ile Glu Arg
1 5 10 15

Arg Val Arg Asp Gly Leu Leu Glu Ile Gly Arg Ala Leu Asn Ile Pro
20 25 30

Pro Leu

<210> 79

<211> 46

<212> PRT

<213> Escherichia coli

<400> 79

Asn Lys Arg Arg Ala Lys Asn Gly Glu Pro Pro Leu Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Lys Lys Ser Phe Asp Met Leu Gln Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
35 40 45

<210> 80

<211> 46

<212> PRT

<213> Vibrio cholerae

<400> 80

Asn Pro Arg Leu Lys Lys Ala Gly Lys Pro Pro Val Arg Ile Glu Ala
1 5 10 15

Ile Pro Leu Asp Asp Ala Arg Ser Phe Arg Asn Leu Gln Asp Ala Lys
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu
35 40 45

<210> 81

<211> 46

<212> PRT

<213> Haemophilus influenzae

<400> 81

Asn Val Arg Met Val Arg Glu Gly Lys Pro Arg Val Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Pro Glu Ser Phe Glu Leu Leu Lys Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
35 40 45

<210> 82

<211> 46

<212> PRT

<213> Rickettsia prowazekii

<400> 82

Cys Lys Lys Leu Leu Lys Glu Gln Gly Ile Lys Ile Asp Phe Asp Asp
1 5 10 15

Met Thr Phe Asp Asp Lys Lys Thr Tyr Gln Met Leu Cys Lys Gly Lys
20 25 30

Gly Val Gly Val Phe Gln Phe Glu Ser Ile Gly Met Lys Asp
35 40 45

<210> 83

<211> 45

<212> PRT

<213> Helicobacter pylori

<400> 83

Leu Lys Ile Ile Lys Thr Gln His Lys Ile Ser Val Asp Phe Leu Ser
1 5 10 15

Leu Asp Met Asp Asp Pro Lys Val Tyr Lys Thr Ile Gln Ser Gly Asp
20 25 30

Thr Val Gly Ile Phe Gln Ile Glu Ser Gly Met Phe Gln
35 40 45

<210> 84

<211> 46

<212> PRT

<213> Synechocystis sp.

<400> 84

Gln Glu Arg Lys Ala Leu Gln Ile Arg Ala Arg Thr Gly Ser Lys Lys
1 5 10 15

Leu Pro Asp Asp Val Lys Lys Thr His Lys Leu Leu Glu Ala Gly Asp
20 25 30

Leu Glu Gly Ile Phe Gln Leu Glu Ser Gln Gly Met Lys Gln
35 40 45

<210> 85

<211> 46

<212> PRT

<213> Mycobacterium tuberculosis

<400> 85

Ile Asp Asn Val Arg Ala Asn Arg Gly Ile Asp Leu Asp Leu Glu Ser
1 5 10 15

Val Pro Leu Asp Asp Lys Ala Thr Tyr Glu Leu Leu Gly Arg Gly Asp
20 25 30

Thr Leu Gly Val Phe Gln Leu Asp Gly Gly Pro Met Arg Asp
35 40 45

<210> 86

<211> 3729

<212> DNA

<213> Thermus thermophilus

<400> 86

atgggcccggg agctccgctt cgccacctc caccagcaca cccagttctc cctcctggac 60
ggggcggcga agctttccga cctcctcaag tgggtcaagg agacgacccc cgaggacccc 120
gccttgcca tgaccgacca cggcaacctc ttcggggcgg tggagttcta caagaaggcc 180
accgaaatgg gcatcaagcc catcctgggc tacgaggcct acgtggcggc ggaaagccgc 240
tttgaccgca agcggggaaa gggcctagac gggggctact ttcacctcac cctcctcgcc 300
aaggacttca cggggtacca gaacctggtg cgcttgccga gccgggctta cctggagggg 360
ttttacgaaa agccccggat tgaccgggag atcctgcgcg agcacgccga gggcctcatc 420
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cccttttgg

3729

<210> 87

<211> 1245

<212> PRT

<213> *Thermus thermophilus*

<400> 87

Met Gly Arg Glu Leu Arg Phe Ala His Leu His Gln His Thr Gln Phe
1 5 10 15

Ser Leu Leu Asp Gly Ala Pro Lys Leu Ser Asp Leu Leu Lys Trp Val
20 25 30

Glu Glu Thr Thr Pro Glu Asp Pro Ala Leu Ala Met Thr Asp His Gly
35 40 45

Asn Leu Phe Gly Ala Val Glu Phe Tyr Lys Lys Ala Thr Glu Met Gly
50 55 60

Ile Lys Pro Ile Leu Gly Tyr Glu Ala Tyr Val Ala Ala Glu Ser Arg
65 70 75 80

Phe Asp Arg Lys Arg Gly Lys Gly Leu Asp Gly Gly Tyr Phe His Leu
85 90 95

Thr Leu Leu Ala Lys Asp Phe Thr Gly Tyr Gln Asn Leu Val Arg Leu
100 105 110

Ala Ser Arg Ala Tyr Leu Glu Gly Phe Tyr Glu Lys Pro Arg Ile Asp
115 120 125

Arg Glu Ile Leu Arg Glu His Ala Glu Gly Leu Ile Ala Leu Ser Gly
130 135 140

Cys Leu Gly Ala Glu Ile Pro Gln Phe Ile Leu Gln Asp Arg Leu Asp
145 150 155 160

Leu Ala Glu Ala Arg Leu Asn Glu Tyr Leu Ser Ile Phe Lys Asp Arg
165 170 175

Phe Phe Ile Glu Ile Gln Asn His Gly Leu Pro Glu Gln Lys Lys Val
180 185 190

Asn Glu Val Leu Lys Glu Phe Ala Arg Lys Tyr Gly Leu Gly Met Val
195 200 205

Ala Thr Asn Asp Gly His Tyr Val Arg Lys Glu Asp Ala Arg Ala His
 210 215 220
 Glu Val Leu Leu Ala Ile Gln Ser Lys Ser Thr Leu Asp Asp Pro Gly
 225 230 235 240
 Ala Leu Ala Leu Pro Cys Glu Glu Phe Tyr Val Lys Thr Pro Glu Glu
 245 250 255
 Met Arg Ala Met Phe Pro Glu Glu Glu Val Gly Gly Arg Ser Pro Leu
 260 265 270
 Thr Thr Pro Trp Arg Ser Pro His Val Gln Arg Gly Ala Ala Ile Gly
 275 280 285
 Thr Arg Trp Ser Thr Arg Ile Pro Arg Phe Pro Leu Pro Glu Gly Arg
 290 295 300
 Thr Glu Ala Gln Tyr Leu Met Glu Leu Thr Phe Lys Gly Leu Leu Arg
 305 310 315 320
 Arg Tyr Pro Asp Arg Ile Thr Glu Gly Phe Tyr Arg Glu Val Phe Arg
 325 330 335
 Leu Ser Gly Lys Leu Pro Pro His Gly Asp Gly Glu Ala Leu Ala Glu
 340 345 350
 Ala Leu Ala Gln Val Glu Arg Glu Ala Trp Glu Arg Leu Met Lys Ser
 355 360 365
 Leu Pro Pro Leu Ala Gly Val Lys Glu Trp Thr Ala Glu Ala Ile Phe
 370 375 380
 His Arg Ala Leu Tyr Glu Leu Ser Ala Ile Glu Arg Met Gly Phe Pro
 385 390 395 400
 Gly Leu Leu Pro His Arg Pro Gly Leu His Gln Leu Gly Pro Glu Lys
 405 410 415
 Gly Val Ser Val Gly Pro Gly Arg Gly Gly Ala Ala Gly Ser Leu Val
 420 425 430
 Ala Tyr Ala Val Gly Ile Thr Asn Ile Asp Pro Leu Arg Phe Gly Leu
 435 440 445
 Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp Ile
 450 455 460

Asp	Thr	Asp	Phe	Ser	Asp	Arg	Glu	Arg	Asp	Arg	Val	Ile	Gln	Tyr	Val	465	470	475	480
Arg	Glu	Arg	Tyr	Gly	Glu	Asp	Lys	Val	Ala	Gln	Ile	Gly	Thr	Leu	Gly	485	490	495	
Ser	Leu	Ala	Ser	Lys	Ala	Ala	Leu	Lys	Glu	Val	Ala	Arg	Val	Tyr	Gly	500	505	510	
Ile	Pro	Arg	Lys	Lys	Ala	Glu	Glu	Leu	Ala	Lys	Leu	Ile	Pro	Val	Gln	515	520	525	
Phe	Gly	Lys	Pro	Lys	Pro	Leu	Gln	Glu	Ala	Ile	Gln	Val	Val	Pro	Glu	530	535	540	
Leu	Arg	Ala	Glu	Met	Glu	Lys	Asp	Pro	Lys	Val	Arg	Glu	Val	Leu	Glu	545	550	555	560
Val	Ala	Met	Arg	Leu	Glu	Gly	Leu	Asn	Arg	His	Ala	Ser	Val	His	Ala	565	570	575	
Gly	Arg	Gly	Gly	Val	Phe	Ser	Glu	Pro	Leu	Thr	Asp	Leu	Val	Pro	Leu	580	585	590	
Cys	Ala	Thr	Arg	Lys	Gly	Gly	Pro	Tyr	Thr	Gln	Tyr	Asp	Met	Gly	Ala	595	600	605	
Val	Glu	Ala	Leu	Gly	Leu	Leu	Lys	Met	Asp	Phe	Leu	Gly	Leu	Arg	Thr	610	615	620	
Leu	Thr	Phe	Leu	Asp	Glu	Val	Lys	Arg	Ile	Val	Lys	Ala	Ser	Gln	Gly	625	630	635	640
Val	Glu	Leu	Asp	Tyr	Asp	Ala	Leu	Pro	Leu	Asp	Asp	Pro	Lys	Thr	Phe	645	650	655	
Ala	Leu	Leu	Ser	Arg	Gly	Glu	Thr	Lys	Gly	Val	Phe	Gln	Leu	Glu	Ser	660	665	670	
Gly	Gly	Met	Thr	Ala	Thr	Leu	Arg	Gly	Leu	Lys	Pro	Arg	Arg	Phe	Glu	675	680	685	
Asp	Leu	Ile	Ala	Ile	Leu	Ser	Leu	Tyr	Arg	Pro	Gly	Pro	Met	Glu	His	690	695	700	
Ile	Pro	Thr	Tyr	Ile	Arg	Arg	His	His	Gly	Leu	Glu	Pro	Val	Ser	Tyr	705	710	715	720

Ser Glu Phe Pro His Ala Glu Lys Tyr Leu Lys Pro Ile Leu Asp Glu
 725 730 735
 Thr Tyr Gly Ile Pro Val Tyr Gln Glu Gln Ile Met Gln Ile Ala Ser
 740 745 750
 Ala Val Ala Gly Tyr Ser Leu Gly Glu Ala Asp Leu Leu Arg Arg Ser
 755 760 765
 Met Gly Lys Lys Lys Val Glu Glu Met Lys Ser His Arg Glu Arg Phe
 770 775 780
 Val Gln Gly Ala Lys Glu Arg Gly Val Pro Glu Glu Glu Ala Asn Arg
 785 790 795 800
 Leu Phe Asp Met Leu Glu Ala Phe Ala Asn Tyr Gly Phe Asn Lys Ser
 805 810 815
 His Ala Ala Ala Tyr Ser Leu Leu Ser Tyr Gln Thr Ala Tyr Val Lys
 820 825 830
 Ala His Tyr Pro Val Glu Phe Met Ala Ala Leu Leu Ser Val Glu Arg
 835 840 845
 His Asp Ser Asp Lys Val Ala Glu Tyr Ile Arg Asp Ala Arg Ala Met
 850 855 860
 Gly Ile Glu Val Leu Pro Pro Asp Val Asn Arg Ser Gly Phe Asp Phe
 865 870 875 880
 Leu Val Gln Gly Arg Gln Ile Leu Phe Gly Leu Ser Ala Val Lys Asn
 885 890 895
 Val Gly Glu Ala Ala Ala Glu Ala Ile Leu Arg Glu Arg Glu Arg Gly
 900 905 910
 Gly Pro Tyr Arg Ser Leu Gly Asp Phe Leu Lys Arg Leu Asp Glu Lys
 915 920 925
 Val Leu Asn Lys Arg Thr Leu Glu Ser Leu Ile Lys Ala Gly Ala Leu
 930 935 940
 Asp Gly Phe Gly Glu Arg Ala Arg Leu Leu Ala Ser Leu Glu Gly Leu
 945 950 955 960
 Leu Lys Trp Ala Ala Glu Asn Arg Glu Lys Ala Arg Ser Gly Met Met
 965 970 975

Gly Leu Phe Ser Glu Val Glu Glu Pro Pro Leu Ala Glu Ala Ala Pro
 980 985 990

Leu Asp Glu Ile Thr Arg Leu Arg Tyr Glu Lys Glu Ala Leu Gly Ile
 995 1000 1005

Tyr Val Ser Gly His Pro Ile Leu Arg Tyr Pro Gly Leu Arg Glu Thr
 1010 1015 1020

Ala Thr Cys Thr Leu Glu Glu Leu Pro His Leu Ala Arg Asp Leu Pro
 1025 1030 1035 1040

Pro Arg Ser Arg Val Leu Leu Ala Gly Met Val Glu Glu Val Val Arg
 1045 1050 1055

Lys Pro Thr Lys Ser Gly Gly Met Met Ala Arg Phe Val Leu Ser Asp
 1060 1065 1070

Glu Thr Gly Ala Leu Glu Ala Val Ala Phe Gly Arg Ala Tyr Asp Gln
 1075 1080 1085

Val Ser Pro Arg Leu Lys Glu Asp Thr Pro Val Leu Val Leu Ala Glu
 1090 1095 1100

Val Glu Arg Glu Glu Gly Gly Val Arg Val Leu Ala Gln Ala Val Trp
 1105 1110 1115 1120

Thr Tyr Gln Glu Leu Glu Gln Val Pro Arg Ala Leu Glu Val Glu Val
 1125 1130 1135

Glu Ala Ser Leu Pro Asp Asp Arg Gly Val Ala His Leu Lys Ser Leu
 1140 1145 1150

Leu Asp Glu His Ala Gly Thr Leu Pro Leu Tyr Val Arg Val Gln Gly
 1155 1160 1165

Ala Phe Gly Glu Ala Leu Leu Ala Leu Arg Glu Val Arg Val Gly Glu
 1170 1175 1180

Glu Ala Leu Gly Ala Leu Glu Ala Ala Gly Phe Pro Ala Tyr Leu Leu
 1185 1190 1195 1200

Pro Asn Arg Glu Val Ser Pro Arg Leu Thr Gly Ser Gly Gly Pro Arg
 1205 1210 1215

Gly Arg Ala Leu Ser Thr Gly Leu Ala Leu Lys Thr Tyr Pro Ile Ala
 1220 1225 1230

Leu Pro Gly Gly Asn Glu Ala Leu Ala Arg Pro Leu Leu
1235 1240 1245

<210> 88
<211> 198
<212> PRT
<213> *Thermus thermophilus*

<400> 88
Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu Glu
1 5 10 15
Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu Gly
20 25 30
Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly Leu
35 40 45
Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg Arg
50 55 60
Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala Arg
65 70 75 80
Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala Pro
85 90 95
Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp Ala
100 105 110
Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg Pro
115 120 125
Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp Ser
130 135 140
Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly Leu
145 150 155 160
Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His Arg
165 170 175
Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val Tyr
180 185 190
Tyr Met Leu Thr Ser Gly
195

<210> 89
 <211> 182
 <212> PRT
 <213> Deinococcus radiodurans

<220>
 <221> PEPTIDE
 <222> (79)
 <223> X at position 79 is undefined

<400> 89
 Pro Trp Pro Gln Asp Val Val Val Phe Asp Leu Glu Thr Thr Gly Phe
 1 5 10 15
 Ser Pro Ala Ser Ala Ala Ile Val Glu Ile Gly Ala Val Arg Ile Val
 20 25 30
 Gly Gly Gln Ile Asp Glu Thr Leu Lys Phe Glu Thr Leu Val Arg Pro
 35 40 45
 Thr Arg Pro Asp Gly Ser Met Leu Ser Ile Pro Trp Gln Ala Gln Arg
 50 55 60
 Val His Gly Ile Ser Asp Glu Met Val Arg Arg Ala Pro Ala Xaa Lys
 65 70 75 80
 Asp Val Leu Pro Asp Phe Phe Asp Phe Val Asp Gly Ser Ala Val Val
 85 90 95
 Ala His Asn Val Ser Phe Asp Gly Gly Phe Met Arg Ala Gly Ala Glu
 100 105 110
 Arg Leu Gly Leu Ser Trp Ala Pro Glu Arg Glu Leu Cys Thr Met Gln
 115 120 125
 Leu Ser Arg Arg Ala Phe Pro Arg Glu Arg Thr His Asn Leu Thr Val
 130 135 140
 Leu Ala Glu Arg Leu Gly Leu Glu Phe Ala Pro Gly Gly Arg His Arg
 145 150 155 160
 Ser Tyr Gly Asp Val Gln Val Thr Ala Gln Ala Tyr Leu Arg Leu Leu
 165 170 175
 Glu Leu Leu Gly Glu Arg
 180

<210> 90
 <211> 201
 <212> PRT
 <213> Bacillus subtilis

<400> 90
 His Gly Ile Lys Met Ile Tyr Gly Met Glu Ala Asn Leu Val Asp Asp
 1 5 10 15
 Gly Val Pro Ile Ala Tyr Asn Ala Ala His Arg Leu Leu Glu Glu Glu
 20 25 30
 Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val Tyr
 35 40 45
 Asp Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Gly Gly Glu Ile
 50 55 60
 Ile Asp Lys Phe Glu Ala Phe Ala Asn Pro His Arg Pro Leu Ser Ala
 65 70 75 80
 Thr Ile Ile Glu Leu Thr Gly Ile Thr Asp Asp Met Leu Gln Asp Ala
 85 90 95
 Pro Asp Val Val Asp Val Ile Arg Asp Phe Arg Glu Trp Ile Gly Asp
 100 105 110
 Asp Ile Leu Val Ala His Asn Ala Ser Phe Asp Met Gly Phe Leu Asn
 115 120 125
 Val Ala Tyr Lys Lys Leu Leu Glu Val Glu Lys Ala Lys Asn Pro Val
 130 135 140
 Ile Asp Thr Leu Glu Leu Gly Arg Phe Leu Tyr Pro Glu Phe Lys Asn
 145 150 155 160
 His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
 165 170 175
 His His Arg Ala Ile Tyr Asp Thr Glu Ala Thr Ala Tyr Leu Leu Leu
 180 185 190
 Lys Met Leu Lys Asp Ala Ala Glu Lys
 195 200

<210> 91
 <211> 188
 <212> PRT
 <213> Haemophilus influenzae

<220>
 <221> PEPTIDE
 <222> (47)
 <223> X at position 47 is undefined

<220>
 <221> PEPTIDE
 <222> (57)
 <223> X at position 57 is undefined

<400> 91
 Met Ile Asn Pro Asn Arg Gln Ile Val Leu Asp Thr Glu Thr Thr Gly
 1 5 10 15
 Met Asn Gln Leu Gly Ala His Tyr Glu Gly His Cys Ile Ile Glu Ile
 20 25 30
 Gly Ala Val Glu Leu Ile Asn Arg Arg Tyr Thr Gly Asn Asn Xaa His
 35 40 45
 Ile Tyr Ile Lys Pro Asp Arg Pro Xaa Asp Pro Asp Ala Ile Lys Val
 50 55 60
 His Gly Ile Thr Asp Glu Met Leu Ala Asp Lys Pro Glu Phe Lys Glu
 65 70 75 80
 Val Ala Gln Asp Phe Leu Asp Tyr Ile Asn Gly Ala Glu Leu Leu Ile
 85 90 95
 His Asn Ala Pro Phe Asp Val Gly Phe Met Asp Tyr Glu Phe Arg Lys
 100 105 110
 Leu Asn Leu Asn Val Lys Thr Asp Asp Ile Cys Leu Val Thr Asp Thr
 115 120 125
 Leu Gln Met Ala Arg Gln Met Tyr Pro Gly Lys Arg Asn Asn Leu Asp
 130 135 140
 Ala Leu Cys Asp Arg Leu Gly Ile Asp Asn Ser Lys Arg Thr Leu His
 145 150 155 160
 Gly Ala Leu Leu Asp Ala Glu Ile Leu Ala Asp Val Tyr Leu Met Met
 165 170 175

Thr Gly Gly Gln Thr Asn Leu Phe Asp Glu Glu Glu
180 185

<210> 92
<211> 189
<212> PRT
<213> Escherichia coli

<400> 92
Met Ser Thr Ala Ile Thr Arg Gln Ile Val Leu Asp Thr Glu Thr Thr
1 5 10 15
Gly Met Asn Gln Ile Gly Ala His Ser Glu Gly His Lys Ile Ile Glu
20 25 30
Ile Gly Ala Val Glu Val Val Asn Arg Arg Leu Thr Gly Asn Asn Phe
35 40 45
His Val Tyr Leu Lys Asp Arg Leu Val Asp Pro Glu Ala Phe Gly Val
50 55 60
His Gly Ile Ala Val Asp Phe Leu Leu Asp Lys Pro Thr Phe Ala Glu
65 70 75 80
Val Ala Val Glu Phe Met Asp Tyr Ile Arg Gly Ala Glu Leu Val Ile
85 90 95
His Asn Ala Ala Phe Asp Ile Gly Phe Met Asp Tyr Glu Phe Ser Leu
100 105 110
Leu Lys Arg Asp Ile Ala Lys Thr Asn Thr Phe Cys Lys Val Thr Asp
115 120 125
Ser Leu Ala Val Ala Arg Lys Met Phe Pro Gly Lys Arg Asn Ser Leu
130 135 140
Asp Ala Leu Cys Ala Arg Tyr Glu Ile Asp Asn Ser Lys Arg Thr Leu
145 150 155 160
His Gly Ala Leu Leu Asp Ala Gln Ile Leu Ala Glu Val Tyr Leu Ala
165 170 175
Met Thr Gly Gly Gln Thr Ser Met Ala Phe Ala Met Glu
180 185

<210> 93
 <211> 201
 <212> PRT
 <213> Helicobacter pylori

<400> 93
 Asn Leu Glu Tyr Leu Lys Ala Cys Gly Leu Asn Phe Ile Glu Thr Ser
 1 5 10 15
 Glu Asn Leu Ile Thr Leu Lys Asn Leu Lys Thr Pro Leu Lys Asp Glu
 20 25 30
 Val Phe Ser Phe Ile Asp Leu Glu Thr Thr Gly Ser Cys Pro Ile Lys
 35 40 45
 His Glu Ile Leu Glu Ile Gly Ala Val Gln Val Lys Gly Gly Glu Ile
 50 55 60
 Ile Asn Arg Phe Glu Thr Leu Val Lys Val Lys Ser Val Pro Asp Tyr
 65 70 75 80
 Ile Ala Glu Leu Thr Gly Ile Thr Tyr Glu Asp Thr Leu Asn Ala Pro
 85 90 95
 Ser Ala His Glu Ala Leu Gln Glu Leu Arg Leu Phe Leu Gly Asn Ser
 100 105 110
 Val Phe Val Ala His Asn Ala Asn Phe Asp Tyr Asn Phe Leu Gly Arg
 115 120 125
 Tyr Phe Val Glu Lys Leu His Cys Pro Leu Leu Asn Leu Lys Leu Cys
 130 135 140
 Thr Leu Asp Leu Ser Lys Arg Ala Ile Leu Ser Met Arg Tyr Ser Leu
 145 150 155 160
 Ser Phe Leu Lys Glu Leu Leu Gly Phe Gly Ile Glu Val Ser His Arg
 165 170 175
 Ala Tyr Ala Asp Ala Leu Ala Ser Tyr Lys Leu Phe Glu Ile Cys Leu
 180 185 190
 Leu Asn Leu Pro Ser Tyr Ile Lys Thr
 195 200

<210> 94
 <211> 630

<212> DNA

<213> *Thermus thermophilus*

<400> 94

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ctggagacca cggggcttgc cggcctggac gaggtgattg aggtgggcct cctccgcctg 180
gaggggggga gggcctccc ctccagagc ctcgcccggc ccctcccgcc cgccgaagcc 240
cgttcgtgga acctcaccgg catcccccg gaggccttg aggaggcccc ctccctggag 300
gaggttcttg agaaggccta cccctccgc ggcgacgcca ccttggtgat ccacaacgcc 360
gcctttgacc tgggcttct cgcgccggc ttggagggcc tgggctaccg cctggaaaac 420
cccggtgttg actccctgcg cttggccaga cggggcttac caggccttag gcgctacggc 480
ctggacgccc tctccgaggt cctggagctt cccgaagga cctgccaccg ggccctcgag 540
gacgtggagc gcaccctcgc cgtggtgcac gaggtatact atatgcttac gtccggccgt 600
ccccgcacgc tttgggaact cgggaggtag                                     630
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<210> 95

<211> 210

<212> PRT

<213> *Thermus thermophilus*

<400> 95

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Met Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu
  1                   5                   10                   15

Glu Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu
                   20                   25                   30

Gly Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly
                   35                   40                   45

Leu Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg
                   50                   55                   60

Arg Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala
                   65                   70                   75                   80

Arg Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala
                   85                   90                   95

Pro Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp
                   100                  105                  110

Ala Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg
                   115                  120                  125

Pro Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp
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130	135	140
Ser Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly		
145	150	155 160
Leu Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His		
	165	170 175
Arg Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val		
	180	185 190
Tyr Tyr Met Leu Thr Ser Gly Arg Pro Arg Thr Leu Trp Glu Leu Gly		
	195	200 205
Arg Glx		
210		
<210> 96		
<211> 461		
<212> PRT		
<213> Pseudomonas marcesans		
<400> 96		
Met Leu Glu Ala Ser Trp Glu Lys Val Gln Ser Ser Leu Lys Gln Asn		
1	5	10 15
Leu Ser Lys Pro Ser Tyr Glu Thr Trp Ile Arg Pro Thr Glu Phe Ser		
	20	25 30
Gly Phe Lys Asn Gly Glu Leu Thr Leu Ile Ala Pro Asn Ser Phe Ser		
	35	40 45
Ser Ala Trp Leu Lys Asn Asn Tyr Ser Gln Thr Ile Gln Glu Thr Ala		
	50	55 60
Glu Glu Ile Phe Gly Glu Pro Val Thr Val His Val Lys Val Lys Ala		
65	70	75 80
Asn Ala Glu Ser Ser Asp Glu His Tyr Ser Ser Ala Pro Ile Thr Pro		
	85	90 95
Pro Leu Glu Ala Ser Pro Gly Ser Val Asp Ser Ser Gly Ser Ser Leu		
	100	105 110
Arg Leu Ser Lys Lys Thr Leu Pro Leu Leu Asn Leu Arg Tyr Val Phe		
	115	120 125

Asn	Arg	Phe	Val	Val	Gly	Pro	Asn	Ser	Arg	Met	Ala	His	Ala	Ala	Ala		
130						135					140						
Met	Ala	Val	Ala	Glu	Ser	Pro	Gly	Arg	Glu	Phe	Asn	Pro	Leu	Phe	Ile		
145					150					155					160		
Cys	Gly	Gly	Val	Gly	Leu	Gly	Lys	Thr	His	Leu	Met	Gln	Ala	Ile	Gly		
				165					170					175			
His	Tyr	Arg	Leu	Glu	Ile	Asp	Pro	Gly	Ala	Lys	Val	Ser	Tyr	Val	Ser		
			180					185					190				
Thr	Glu	Thr	Phe	Thr	Asn	Asp	Leu	Ile	Leu	Ala	Ile	Arg	Gln	Asp	Arg		
		195					200					205					
Met	Gln	Ala	Phe	Arg	Asp	Arg	Tyr	Arg	Ala	Ala	Asp	Leu	Ile	Leu	Val		
	210					215					220						
Asp	Asp	Ile	Gln	Phe	Ile	Glu	Gly	Lys	Glu	Tyr	Thr	Gln	Glu	Glu	Phe		
225					230					235					240		
Phe	His	Thr	Phe	Asn	Ala	Leu	His	Asp	Ala	Gly	Ser	Gln	Ile	Val	Leu		
				245					250			.		255			
Ala	Ser	Asp	Arg	Pro	Pro	Ser	Gln	Ile	Pro	Arg	Leu	Gln	Glu	Arg	Leu		
			260					265					270				
Met	Ser	Arg	Phe	Ser	Met	Gly	Leu	Ile	Ala	Asp	Val	Gln	Ala	Pro	Asp		
		275					280					285					
Leu	Glu	Thr	Arg	Met	Ala	Ile	Leu	Gln	Lys	Lys	Ala	Glu	His	Glu	Arg		
	290					295					300						
Val	Gly	Leu	Pro	Arg	Asp	Leu	Ile	Gln	Phe	Ile	Ala	Gly	Arg	Phe	Thr		
305					310					315					320		
Ser	Asn	Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Thr	Arg	Ala	Ile	Ala	Phe		
				325					330					335			
Ala	Ser	Ile	Thr	Gly	Leu	Pro	Met	Thr	Val	Asp	Ser	Ile	Ala	Pro	Met		
			340					345					350				
Leu	Asp	Pro	Asn	Gly	Gln	Gly	Val	Glu	Val	Thr	Pro	Lys	Gln	Val	Leu		
		355					360					365					
Asp	Lys	Val	Ala	Glu	Val	Phe	Lys	Val	Thr	Pro	Asp	Glu	Met	Arg	Ser		
	370					375					380						

Ala Ser Arg Arg Arg Pro Val Ser Gln Ala Arg Gln Val Gly Met Tyr
 385 390 395 400

Leu Met Arg Gln Gly Thr Asn Leu Ser Leu Pro Arg Ile Gly Asp Thr
 405 410 415

Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ala Ile Glu Gln Val
 420 425 430

Glu Lys Lys Leu Ser Ser Asp Pro Gln Ile Ala Ser Gln Val Gln Lys
 435 440 445

Ile Arg Asp Leu Leu Gln Ile Asp Ser Arg Arg Lys Arg
 450 455 460

<210> 97

<211> 447

<212> PRT

<213> Synechocystis sp.

<400> 97

Met Val Ser Cys Glu Asn Leu Trp Gln Gln Ala Leu Ala Ile Leu Ala
 1 5 10 15

Thr Gln Leu Thr Lys Pro Ala Phe Asp Thr Trp Ile Lys Ala Ser Val
 20 25 30

Leu Ile Ser Leu Gly Asp Gly Val Ala Thr Ile Gln Val Glu Asn Gly
 35 40 45

Phe Val Leu Asn His Leu Gln Lys Ser Tyr Gly Pro Leu Leu Met Glu
 50 55 60

Val Leu Thr Asp Leu Thr Gly Gln Glu Ile Thr Val Lys Leu Ile Thr
 65 70 75 80

Asp Gly Leu Glu Pro His Ser Leu Ile Gly Gln Glu Ser Ser Leu Pro
 85 90 95

Met Glu Thr Thr Pro Lys Asn Ala Thr Ala Leu Asn Gly Lys Tyr Thr
 100 105 110

Phe Ser Arg Phe Val Val Gly Pro Thr Asn Arg Met Ala His Ala Ala
 115 120 125

Ser Leu Ala Val Ala Glu Ser Pro Gly Arg Glu Phe Asn Pro Leu Phe
 130 135 140

Leu Cys Gly Gly Val Gly Leu Gly Lys Thr His Leu Met Gln Ala Ile
 145 150 155 160

Ala His Tyr Arg Leu Glu Met Tyr Pro Asn Ala Lys Val Tyr Tyr Val
 165 170 175

Ser Thr Glu Arg Phe Thr Asn Asp Leu Ile Thr Ala Ile Arg Gln Asp
 180 185 190

Asn Met Glu Asp Phe Arg Ser Tyr Tyr Arg Ser Ala Asp Phe Leu Leu
 195 200 205

Ile Asp Asp Ile Gln Phe Ile Lys Gly Lys Glu Tyr Thr Gln Glu Glu
 210 215 220

Phe Phe His Thr Phe Asn Ser Leu His Glu Ala Gly Lys Gln Val Val
 225 230 235 240

Val Ala Ser Asp Arg Ala Pro Gln Arg Ile Pro Gly Leu Gln Asp Arg
 245 250 255

Leu Ile Ser Arg Phe Ser Met Gly Leu Ile Ala Asp Ile Gln Val Pro
 260 265 270

Asp Leu Glu Thr Arg Met Ala Ile Leu Gln Lys Lys Ala Glu Tyr Asp
 275 280 285

Arg Ile Arg Leu Pro Lys Glu Val Ile Glu Tyr Ile Ala Ser His Tyr
 290 295 300

Thr Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Ile Arg Ala Ile Ala
 305 310 315 320

Tyr Thr Ser Leu Ser Asn Val Ala Met Thr Val Glu Asn Ile Ala Pro
 325 330 335

Val Leu Asn Pro Pro Val Glu Lys Val Ala Ala Ala Pro Glu Thr Ile
 340 345 350

Ile Thr Ile Val Ala Gln His Tyr Gln Leu Lys Val Glu Glu Leu Leu
 355 360 365

Ser Asn Ser Arg Arg Arg Glu Val Ser Leu Ala Arg Gln Val Gly Met
 370 375 380

Tyr Leu Met Arg Gln His Thr Asp Leu Ser Leu Pro Arg Ile Gly Glu
 385 390 395 400

Ala Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ser Cys Asp Lys
405 410 415

Ile Thr Gln Leu Gln Gln Lys Asp Trp Glu Thr Ser Gln Thr Leu Thr
420 425 430

Ser Leu Ser His Arg Ile Asn Ile Ala Gly Gln Ala Pro Glu Ser
435 440 445

<210> 98

<211> 446

<212> PRT

<213> Bacillus subtilis

<400> 98

Met Glu Asn Ile Leu Asp Leu Trp Asn Gln Ala Leu Ala Gln Ile Glu
1 5 10 15

Lys Lys Leu Ser Lys Pro Ser Phe Glu Thr Trp Met Lys Ser Thr Lys
20 25 30

Ala His Ser Leu Gln Gly Asp Thr Leu Thr Ile Thr Ala Pro Asn Glu
35 40 45

Phe Ala Arg Asp Trp Leu Glu Ser Arg Tyr Leu His Leu Ile Ala Asp
50 55 60

Thr Ile Tyr Glu Leu Thr Gly Glu Glu Leu Ser Ile Lys Phe Val Ile
65 70 75 80

Pro Gln Asn Gln Asp Val Glu Asp Phe Met Pro Lys Pro Gln Val Lys
85 90 95

Lys Ala Val Lys Glu Asp Thr Ser Asp Phe Pro Gln Asn Met Leu Asn
100 105 110

Pro Lys Tyr Thr Phe Asp Thr Phe Val Ile Gly Ser Gly Asn Arg Phe
115 120 125

Ala His Ala Ala Ser Leu Ala Val Ala Glu Ala Pro Ala Lys Ala Tyr
130 135 140

Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr His Leu
145 150 155 160

Met His Ala Ile Gly His Tyr Val Ile Asp His Asn Pro Ser Ala Lys

165							170							175						
Val	Val	Tyr	Leu	Ser	Ser	Glu	Lys	Phe	Thr	Asn	Glu	Phe	Ile	Asn	Ser					
			180					185					190							
Ile	Arg	Asp	Asn	Lys	Ala	Val	Asp	Phe	Arg	Asn	Arg	Tyr	Arg	Asn	Val					
			195					200					205							
Asp	Val	Leu	Leu	Ile	Asp	Asp	Ile	Gln	Phe	Leu	Ala	Gly	Lys	Glu	Gln					
			210					215					220							
Thr	Gln	Glu	Glu	Phe	Phe	His	Thr	Phe	Asn	Thr	Leu	His	Glu	Glu	Ser					
225					230					235					240					
Lys	Gln	Ile	Val	Ile	Ser	Ser	Asp	Arg	Pro	Pro	Lys	Glu	Ile	Pro	Thr					
			245					250					255							
Leu	Glu	Asp	Arg	Leu	Arg	Ser	Arg	Phe	Glu	Trp	Gly	Leu	Ile	Thr	Asp					
			260					265					270							
Ile	Thr	Pro	Pro	Asp	Leu	Glu	Thr	Arg	Ile	Ala	Ile	Leu	Arg	Lys	Lys					
			275					280					285							
Ala	Lys	Ala	Glu	Gly	Leu	Asp	Ile	Pro	Asn	Glu	Val	Met	Leu	Tyr	Ile					
			290					295					300							
Ala	Asn	Gln	Ile	Asp	Ser	Asn	Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Ile					
305					310					315					320					
Arg	Val	Val	Ala	Tyr	Ser	Ser	Leu	Ile	Asn	Lys	Asp	Ile	Asn	Ala	Asp					
			325					330					335							
Leu	Ala	Ala	Glu	Ala	Leu	Lys	Asp	Ile	Ile	Pro	Ser	Ser	Lys	Pro	Lys					
			340					345					350							
Val	Ile	Thr	Ile	Lys	Glu	Ile	Gln	Arg	Val	Val	Gly	Gln	Gln	Phe	Asn					
			355					360					365							
Ile	Lys	Leu	Glu	Asp	Phe	Lys	Ala	Lys	Lys	Arg	Thr	Lys	Ser	Val	Ala					
			370					375					380							
Phe	Pro	Arg	Gln	Ile	Ala	Met	Tyr	Leu	Ser	Arg	Glu	Met	Thr	Asp	Ser					
385					390					395					400					
Ser	Leu	Pro	Lys	Ile	Gly	Glu	Glu	Phe	Gly	Gly	Arg	Asp	His	Thr	Thr					
			405					410					415							
Val	Ile	His	Ala	His	Glu	Lys	Ile	Ser	Lys	Leu	Leu	Ala	Asp	Asp	Glu					

420 425 430
 Gln Leu Gln Gln His Val Lys Glu Ile Lys Glu Gln Leu Lys
 435 440 445

 <210> 99
 <211> 507
 <212> PRT
 <213> Mycobacterium tuberculosis

 <400> 99
 Met Thr Asp Asp Pro Gly Ser Gly Phe Thr Thr Val Trp Asn Ala Val
 1 5 10 15

 Val Ser Glu Leu Asn Gly Asp Pro Lys Val Asp Asp Gly Pro Ser Ser
 20 25 30

 Asp Ala Asn Leu Ser Ala Pro Leu Thr Pro Gln Gln Arg Ala Trp Leu
 35 40 45

 Asn Leu Val Gln Pro Leu Thr Ile Val Glu Gly Phe Ala Leu Leu Ser
 50 55 60

 Val Pro Ser Ser Phe Val Gln Asn Glu Ile Glu Arg His Leu Arg Ala
 65 70 75 80

 Pro Ile Thr Asp Ala Leu Ser Arg Arg Leu Gly His Gln Ile Gln Leu
 85 90 95

 Gly Val Arg Ile Ala Pro Pro Ala Thr Asp Glu Ala Asp Asp Thr Thr
 100 105 110

 Val Pro Pro Ser Glu Asn Pro Ala Thr Thr Ser Pro Asp Thr Thr Thr
 115 120 125

 Asp Asn Asp Glu Ile Asp Asp Ser Ala Ala Ala Arg Gly Asp Asn Gln
 130 135 140

 His Ser Trp Pro Ser Tyr Phe Thr Glu Arg Pro His Asn Thr Asp Ser
 145 150 155 160

 Ala Thr Ala Gly Val Thr Ser Leu Asn Arg Arg Tyr Thr Phe Asp Thr
 165 170 175

 Phe Val Ile Gly Ala Ser Asn Arg Phe Ala His Ala Ala Ala Leu Ala
 180 185 190

Ile	Ala	Glu	Ala	Pro	Ala	Arg	Ala	Tyr	Asn	Pro	Leu	Phe	Ile	Trp	Gly	195	200	205	
Glu	Ser	Gly	Leu	Gly	Lys	Thr	His	Leu	Leu	His	Ala	Ala	Gly	Asn	Tyr	210	215	220	
Ala	Gln	Arg	Leu	Phe	Pro	Gly	Met	Arg	Val	Lys	Tyr	Val	Ser	Thr	Glu	225	230	235	240
Glu	Phe	Thr	Asn	Asp	Phe	Ile	Asn	Ser	Leu	Arg	Asp	Asp	Arg	Lys	Val	245	250	255	
Ala	Phe	Lys	Arg	Ser	Tyr	Arg	Asp	Val	Asp	Val	Leu	Leu	Val	Asp	Asp	260	265	270	
Ile	Gln	Phe	Ile	Glu	Gly	Lys	Glu	Gly	Ile	Gln	Glu	Glu	Phe	Phe	His	275	280	285	
Thr	Phe	Asn	Thr	Leu	His	Asn	Ala	Asn	Lys	Gln	Ile	Val	Ile	Ser	Ser	290	295	300	
Asp	Arg	Pro	Pro	Lys	Gln	Leu	Ala	Thr	Leu	Glu	Asp	Arg	Leu	Arg	Thr	305	310	315	320
Arg	Phe	Glu	Trp	Gly	Leu	Ile	Thr	Asp	Val	Gln	Pro	Pro	Glu	Leu	Glu	325	330	335	
Thr	Arg	Ile	Ala	Ile	Leu	Arg	Lys	Lys	Ala	Gln	Met	Glu	Arg	Leu	Ala	340	345	350	
Val	Pro	Asp	Asp	Val	Leu	Glu	Leu	Ile	Ala	Ser	Ser	Ile	Glu	Arg	Asn	355	360	365	
Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Ile	Arg	Val	Thr	Ala	Phe	Ala	Ser	370	375	380	
Leu	Asn	Lys	Thr	Pro	Ile	Asp	Lys	Ala	Leu	Ala	Glu	Ile	Val	Leu	Arg	385	390	395	400
Asp	Leu	Ile	Ala	Asp	Ala	Asn	Thr	Met	Gln	Ile	Ser	Ala	Ala	Thr	Ile	405	410	415	
Met	Ala	Ala	Thr	Ala	Glu	Tyr	Phe	Asp	Thr	Thr	Val	Glu	Glu	Leu	Arg	420	425	430	
Gly	Pro	Gly	Lys	Thr	Arg	Ala	Leu	Ala	Gln	Ser	Arg	Gln	Ile	Ala	Met	435	440	445	

Tyr Leu Cys Arg Glu Leu Thr Asp Leu Ser Leu Pro Lys Ile Gly Gln
 450 455 460

Ala Phe Gly Arg Asp His Thr Thr Val Met Tyr Ala Gln Arg Lys Ile
 465 470 475 480

Leu Ser Glu Met Ala Glu Arg Arg Glu Val Phe Asp His Val Lys Glu
 485 490 495

Leu Thr Thr Arg Ile Arg Gln Arg Ser Lys Arg
 500 505

<210> 100

<211> 446

<212> PRT

<213> Thermus thermophilus

<400> 100

Met Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
 1 5 10 15

Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
 20 25 30

Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
 35 40 45

Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly
 50 55 60

Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val
 65 70 75 80

Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro
 85 90 95

Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly
 100 105 110

Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser
 115 120 125

Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu
 130 135 140

Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg
 145 150 155 160

Phe	Pro	His	Met	Arg	Leu	Glu	Tyr	Val	Ser	Thr	Glu	Thr	Phe	Thr	Asn			
				165					170					175				
Glu	Leu	Ile	Asn	Arg	Pro	Ser	Ala	Arg	Asp	Arg	Met	Thr	Glu	Phe	Arg			
			180					185					190					
Glu	Arg	Tyr	Arg	Ser	Val	Asp	Leu	Leu	Leu	Val	Asp	Asp	Val	Gln	Phe			
		195					200					205						
Ile	Ala	Gly	Lys	Glu	Arg	Thr	Gln	Glu	Glu	Phe	Phe	His	Thr	Phe	Asn			
	210					215					220							
Ala	Leu	Tyr	Glu	Ala	His	Lys	Gln	Ile	Ile	Leu	Ser	Ser	Asp	Arg	Pro			
225					230					235					240			
Pro	Lys	Asp	Ile	Leu	Thr	Leu	Glu	Ala	Arg	Leu	Arg	Ser	Arg	Phe	Glu			
			245						250					255				
Trp	Gly	Leu	Ile	Thr	Asp	Asn	Pro	Ala	Pro	Asp	Leu	Glu	Thr	Arg	Ile			
		260						265					270					
Ala	Ile	Leu	Lys	Met	Asn	Ala	Ser	Ser	Gly	Pro	Glu	Asp	Pro	Glu	Asp			
	275						280					285						
Ala	Leu	Glu	Tyr	Ile	Ala	Arg	Gln	Val	Thr	Ser	Asn	Ile	Arg	Glu	Trp			
	290					295					300							
Glu	Gly	Ala	Leu	Met	Arg	Ala	Ser	Pro	Phe	Ala	Ser	Leu	Asn	Gly	Val			
305					310					315					320			
Glu	Leu	Thr	Arg	Ala	Val	Ala	Ala	Lys	Ala	Leu	Arg	His	Leu	Arg	Pro			
			325					330						335				
Arg	Glu	Leu	Glu	Ala	Asp	Pro	Leu	Glu	Ile	Ile	Arg	Lys	Ala	Ala	Gly			
		340						345					350					
Pro	Val	Arg	Pro	Glu	Thr	Pro	Gly	Gly	Ala	His	Gly	Glu	Arg	Arg	Lys			
		355					360					365						
Lys	Glu	Val	Val	Leu	Pro	Arg	Gln	Leu	Ala	Met	Tyr	Leu	Val	Arg	Glu			
	370					375					380							
Leu	Thr	Pro	Ala	Ser	Leu	Pro	Glu	Ile	Gly	Gln	Leu	Phe	Gly	Gly	Arg			
385					390					395					400			
Asp	His	Thr	Thr	Val	Arg	Tyr	Ala	Ile	Gln	Lys	Val	Gln	Glu	Leu	Ala			
			405						410					415				

Gly Lys Pro Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu
420 425 430

Ala Cys Thr Asp Pro Val Asp Asn Leu Trp Ile Thr Cys Gly
435 440 445

<210> 101

<211> 467

<212> PRT

<213> Escherichia coli

<400> 101

Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu
1 5 10 15

Leu Pro Ala Thr Glu Phe Ser Met Trp Ile Arg Pro Leu Gln Ala Glu
20 25 30

Leu Ser Asp Asn Thr Leu Ala Leu Tyr Ala Pro Asn Arg Phe Val Leu
35 40 45

Asp Trp Val Arg Asp Lys Tyr Leu Asn Asn Ile Asn Gly Leu Leu Thr
50 55 60

Ser Phe Cys Gly Ala Asp Ala Pro Gln Leu Arg Phe Glu Val Gly Thr
65 70 75 80

Lys Pro Val Thr Gln Thr Pro Gln Ala Ala Val Thr Ser Asn Val Ala
85 90 95

Ala Pro Ala Gln Val Ala Gln Thr Gln Pro Gln Arg Ala Ala Pro Ser
100 105 110

Thr Arg Ser Gly Trp Asp Asn Val Pro Ala Pro Ala Glu Pro Thr Tyr
115 120 125

Arg Ser Asn Val Asn Val Lys His Thr Phe Asp Asn Phe Val Glu Gly
130 135 140

Lys Ser Asn Gln Leu Ala Arg Ala Ala Ala Arg Gln Val Ala Asp Asn
145 150 155 160

Pro Gly Gly Ala Tyr Asn Pro Leu Phe Leu Tyr Gly Gly Thr Gly Leu
165 170 175

Gly Lys Thr His Leu Leu His Ala Val Gly Asn Gly Ile Met Ala Arg

180	185	190
Lys Pro Asn Ala Lys Val Val Tyr Met His Ser Glu Arg Phe Val Gln		
195	200	205
Asp Met Val Lys Ala Leu Gln Asn Asn Ala Ile Glu Glu Phe Lys Arg		
210	215	220
Tyr Tyr Arg Ser Val Asp Ala Leu Leu Ile Asp Asp Ile Gln Phe Phe		
225	230	235
Ala Asn Lys Glu Arg Ser Gln Glu Glu Phe Phe His Thr Phe Asn Ala		
245	250	255
Leu Leu Glu Gly Asn Gln Gln Ile Ile Leu Thr Ser Asp Arg Tyr Pro		
260	265	270
Lys Glu Ile Asn Gly Val Glu Asp Arg Leu Lys Ser Arg Phe Gly Trp		
275	280	285
Gly Leu Thr Val Ala Ile Glu Pro Pro Glu Leu Glu Thr Arg Val Ala		
290	295	300
Ile Leu Met Lys Lys Ala Asp Glu Asn Asp Ile Arg Leu Pro Gly Glu		
305	310	315
Val Ala Phe Phe Ile Ala Lys Arg Leu Arg Ser Asn Val Arg Glu Leu		
325	330	335
Glu Gly Ala Leu Asn Arg Val Ile Ala Asn Ala Asn Phe Thr Gly Arg		
340	345	350
Ala Ile Thr Ile Asp Phe Val Arg Glu Ala Leu Arg Asp Leu Leu Ala		
355	360	365
Leu Gln Glu Lys Leu Val Thr Ile Asp Asn Ile Gln Lys Thr Val Ala		
370	375	380
Glu Tyr Tyr Lys Ile Lys Val Ala Asp Leu Leu Ser Lys Arg Arg Ser		
385	390	395
Arg Ser Val Ala Arg Pro Arg Gln Met Ala Met Ala Leu Ala Lys Glu		
405	410	415
Leu Thr Asn His Ser Leu Pro Glu Ile Gly Asp Ala Phe Gly Gly Arg		
420	425	430
Asp His Thr Thr Val Leu His Ala Cys Arg Lys Ile Glu Gln Leu Arg		

435 440 445
 Glu Glu Ser His Asp Ile Lys Glu Asp Phe Ser Asn Leu Ile Arg Thr
 450 455 460

 Leu Ser Ser
 465

 <210> 102
 <211> 440
 <212> PRT
 <213> *Thermatoga maritima*

 <400> 102
 Met Lys Glu Arg Ile Leu Gln Glu Ile Lys Thr Arg Val Asn Arg Lys
 1 5 10 15

 Ser Trp Glu Leu Trp Phe Ser Ser Phe Asp Val Lys Ser Ile Glu Gly
 20 25 30

 Asn Lys Val Val Phe Ser Val Gly Asn Leu Phe Ile Lys Glu Trp Leu
 35 40 45

 Glu Lys Lys Tyr Tyr Ser Val Leu Ser Lys Ala Val Lys Val Val Leu
 50 55 60

 Gly Asn Asp Ala Thr Phe Glu Ile Thr Tyr Glu Ala Phe Glu Pro His
 65 70 75 80

 Ser Ser Tyr Ser Glu Pro Leu Val Lys Lys Arg Ala Val Leu Leu Thr
 85 90 95

 Pro Leu Asn Pro Asp Tyr Thr Phe Glu Asn Phe Val Val Gly Pro Gly
 100 105 110

 Asn Ser Phe Ala Tyr His Ala Ala Leu Glu Val Ala Lys His Pro Gly
 115 120 125

 Arg Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr
 130 135 140

 His Leu Leu Gln Ser Ile Gly Asn Tyr Val Val Gln Asn Glu Pro Asp
 145 150 155 160

 Leu Arg Val Met Tyr Ile Thr Ser Glu Lys Phe Leu Asn Asp Leu Val
 165 170 175

Asp	Ser	Met	Lys	Glu	Gly	Lys	Leu	Asn	Glu	Phe	Arg	Glu	Lys	Tyr	Arg		
			180					185					190				
Lys	Lys	Val	Asp	Ile	Leu	Leu	Ile	Asp	Asp	Val	Gln	Phe	Leu	Ile	Gly		
			195				200					205					
Lys	Thr	Gly	Val	Gln	Thr	Glu	Leu	Phe	His	Thr	Phe	Asn	Glu	Leu	His		
	210					215					220						
Asp	Ser	Gly	Lys	Gln	Ile	Val	Ile	Cys	Ser	Asp	Arg	Glu	Pro	Gln	Lys		
225					230					235					240		
Leu	Ser	Glu	Phe	Gln	Asp	Arg	Leu	Val	Ser	Arg	Phe	Gln	Met	Gly	Leu		
				245					250					255			
Val	Ala	Lys	Leu	Glu	Pro	Pro	Asp	Glu	Glu	Thr	Arg	Lys	Ser	Ile	Ala		
			260					265						270			
Arg	Lys	Met	Leu	Glu	Ile	Glu	His	Gly	Glu	Leu	Pro	Glu	Glu	Val	Leu		
		275					280					285					
Asn	Phe	Val	Ala	Glu	Asn	Val	Asp	Asp	Asn	Leu	Arg	Arg	Leu	Arg	Gly		
	290					295					300						
Ala	Ile	Ile	Lys	Leu	Leu	Val	Tyr	Lys	Glu	Thr	Thr	Gly	Lys	Glu	Val		
305					310					315					320		
Asp	Leu	Lys	Glu	Ala	Ile	Leu	Leu	Leu	Lys	Asp	Phe	Ile	Lys	Pro	Asn		
				325					330					335			
Arg	Val	Lys	Ala	Met	Asp	Pro	Ile	Asp	Glu	Leu	Ile	Glu	Ile	Val	Ala		
			340					345					350				
Lys	Val	Thr	Gly	Val	Pro	Arg	Glu	Glu	Ile	Leu	Ser	Asn	Ser	Arg	Asn		
		355					360					365					
Val	Lys	Ala	Leu	Thr	Ala	Arg	Arg	Ile	Gly	Met	Tyr	Val	Ala	Lys	Asn		
	370					375					380						
Tyr	Leu	Lys	Ser	Ser	Leu	Arg	Thr	Ile	Ala	Glu	Lys	Phe	Asn	Arg	Ser		
385					390					395					400		
His	Pro	Val	Val	Val	Asp	Ser	Val	Lys	Lys	Val	Lys	Asp	Ser	Leu	Leu		
				405					410					415			
Lys	Gly	Asn	Lys	Gln	Leu	Lys	Ala	Leu	Ile	Asp	Glu	Val	Ile	Gly	Glu		
			420					425						430			

Ile Ser Arg Arg Ala Leu Ser Gly
435 440

<210> 103

<211> 457

<212> PRT

<213> Helicobacter pylori

<400> 103

Met Asp Thr Asn Asn Asn Ile Glu Lys Glu Ile Leu Ala Leu Val Lys
1 5 10 15

Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu Asn Tyr Phe Ser Gln
20 25 30

Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp Ile Ala Phe Phe Tyr
35 40 45

Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr Ala Lys Tyr Gly Ala
50 55 60

Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val Gly Met His Leu Ala
65 70 75 80

His Ser Val Asp Val Arg Ile Glu Val Ala Pro Lys Ile Gln Ile Asn
85 90 95

Ala Gln Ser Asn Ile Asn Tyr Lys Ala Ile Lys Thr Ser Val Lys Asp
100 105 110

Ser Tyr Thr Phe Glu Asn Phe Val Val Gly Ser Cys Asn Asn Thr Val
115 120 125

Tyr Glu Ile Ala Lys Lys Val Ala Gln Ser Asp Thr Pro Pro Tyr Asn
130 135 140

Pro Val Leu Phe Tyr Gly Gly Thr Gly Leu Gly Lys Thr His Ile Leu
145 150 155 160

Asn Ala Ile Gly Asn His Ala Leu Glu Lys His Lys Lys Val Val Leu
165 170 175

Val Thr Ser Glu Asp Phe Leu Thr Asp Phe Leu Lys His Leu Asp Asn
180 185 190

Lys Thr Met Asp Ser Phe Lys Ala Lys Tyr Arg His Cys Asp Phe Phe
195 200 205

<210> 104
 <211> 1305
 <212> DNA
 <213> *Thermus thermophilus*

<400> 104
 gtgtcgcacg aggccgtctg gcaacacggt ctggagcaca tccgccgcag catcaccgag 60
 gtggagttcc acacctggtt tgaaaggatc cggcccttgg ggatccggga cggggtgctg 120
 gagctcgccg tgccacctc ctttgccctg gactggatcc ggcgccacta cgccggcctc 180
 atccaggagg gccctcggct cctcggggcc caggcgcccc ggtttgagct ccgggtggtg 240
 cccggggtcg tagtccagga ggacatcttc cagccccgcg cgagcccccc ggcccaagct 300
 caaccgaag ataccttta aacttcgtgg tggggcccaa caactccatg gcccacggc 360
 ggcgcgtgg ccgtggccga gtccccggc cgggcctaca acccctctt catctacggg 420
 ggccgtggcc tgggaaagac ctacctgat cacgcgtgg gccactccg tgcgaagcgc 480
 tccccccaca tgagattaga gtacgtttcc acggaactt tcaccaacga gctcatcaac 540
 cggccatccg cgagggaccg gatgacggag ttccgggagc ggtaccgctc cgtggacctc 600
 ctgctggtgg acgacgtcca gttcatcgcc ggaaaggagc gcaccagga ggagtttttc 660
 cacaccttca acgcccccca cgaggccac aagcagatca tcctctctc cgaccggccg 720
 cccaaggaca tcctcaccct ggaggcgcgc ctgcgagacc gctttgagtg gggcctgac 780
 accgacaatc cagccccga cctggaaacc cggatcgcca tcctgaagat gaacgccagc 840
 agcgggcctg aggatcccga ggacgcctg gactacatcg cccggcaggt cacctccaac 900
 atccgggagt ggggaagggc cctcatgcgg gcatcgctt tcgcctccct caacggcgtt 960
 gagctgaccc gcgcgtggc ggccaaggct ctccgacatc ttgcgccag ggagctggag 1020
 gcggaccctt tggagatcat ccgcaaagcg gcgggaccag ttcggcctga aaccgggga 1080
 ggagctcacg gggagcggc caagaaggag gtggtcctcc cccggcagct cgccatgtac 1140
 ctggtgcggg agctcaccg ggcctccctg cccgagatcg accagctcaa cgacgaccgg 1200
 gaccacacca cggctcctta cgccatccag aaggtccagg agctcgcgga aagcgaccgg 1260
 gaggtgcagg gcctcctccg caccctccg gaggcgtgca catga 1305

<210> 105
 <211> 434
 <212> PRT
 <213> *Thermus thermophilus*

<400> 105
 Val Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
 1 5 10 15
 Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
 20 25 30
 Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
 35 40 45
 Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly

50	55	60
Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val		
65	70	75 80
Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro		
	85	90 95
Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly		
	100	105 110
Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser		
	115	120 125
Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu		
130	135	140
Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg		
145	150	155 160
Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn		
	165	170 175
Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg		
	180	185 190
Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe		
	195	200 205
Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn		
210	215	220
Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro		
225	230	235 240
Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu		
	245	250 255
Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile		
	260	265 270
Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp		
	275	280 285
Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp		
290	295	300
Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val		

305 310 315 320
 Glu Leu Thr Arg Ala Val Ala Ala Lys Ala Leu Arg His Leu Arg Pro
 325 330 335
 Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly
 340 345 350
 Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys
 355 360 365
 Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu
 370 375 380
 Leu Thr Pro Ala Ser Leu Pro Glu Ile Asp Gln Leu Asn Asp Asp Arg
 385 390 395 400
 Asp His Thr Thr Val Leu Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala
 405 410 415
 Glu Ser Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu Ala
 420 425 430

Cys Thr

<210> 106
 <211> 1128
 <212> DNA
 <213> *Thermus thermophilus*

<400> 106
 atgaacataa cgggttcccaa aaaactcctc tcggaccagc tttccctcct ggagcgcatac 60
 gtccccctcta gaagcgccaa ccccctctac acctacctgg ggctttacgc cgaggaaggg 120
 gccttgatcc tcttcgggac caacggggag gtggacctcg aggtccgcct ccccgccgag 180
 gcccaaagcc ttccccgggt gctcgtcccc gccagccct tcttcagct ggtgcgagc 240
 cttcctgggg acctcgtggc cctcggcctc gcctcggagc cgggccaggg ggggcagctg 300
 gagctctcct ccgggcgttt ccgcaccggt ctcagcctgg cccctgccga gggctacccc 360
 gagcttcttg tgcccagagg ggaggacaag ggggccttcc ccctccggac gcgcatgccc 420
 tccggggagc tcgtcaaggc cttgaccac gtgcgtacg ccgcgagcaa cgaggagtac 480
 cgggccatct tccgcggggt gcagctggag ttctcccccc agggcttccg ggcggtggcc 540
 tccgacgggt accgcctcgc cctctacgac ctgcccctgc cccaagggtt ccaggccaag 600
 gccgtggtcc ccgcccggag cgtggacgag atggtgctgg tcctgaaggg ggcggacggg 660
 gccgaggccg tcctcgccct gggcgagggg gtgttgggcc tggccctcga gggcggaagc 720
 ggggtccgga tggccctccg cctcatggaa ggggagttcc ccgactacca gagggtcatac 780
 ccccaggagt tcgccctcaa ggtccaggtg gagggggagg ccctcaggga ggcggtgcgc 840
 cgggtgagcg tcctctccga ccggcagaac caccgggtgg acctcctttt ggaggaaggc 900

cggatcctcc tctccgccga gggggactac ggcaaggggc aggaggaggt gcccgccag 960
 gtggaggggc cggacatggc cgtggcctac aacgccgct acctcctcga ggccctcgcc 1020
 cccgtggggg accgggccc cctgggcata tccgggccc cgagcccag cctcatctgg 1080
 ggggacgggg aggggtaccg ggcggtggtg gtgccoctca ggggtctag 1128

<210> 107

<211> 376

<212> PRT

<213> *Thermus thermophilus*

<400> 107

Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
 1 5 10 15

Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
 20 25 30

Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn
 35 40 45

Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu
 50 55 60

Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser
 65 70 75 80

Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln
 85 90 95

Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser
 100 105 110

Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu
 115 120 125

Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu
 130 135 140

Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr
 145 150 155 160

Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe
 165 170 175

Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro
 180 185 190

Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
 195 200 205

Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val
 210 215 220

Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser
 225 230 235 240

Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr
 245 250 255

Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly
 260 265 270

Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg
 275 280 285

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
 290 295 300

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
 305 310 315 320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
 325 330 335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
 340 345 350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
 355 360 365

Val Val Val Pro Leu Arg Val Glx
 370 375

<210> 108

<211> 376

<212> PRT

<213> Thermus thermophilus

<400> 108

Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
 1 5 10 15

Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
 20 25 30

Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn
 35 40 45
 Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu
 50 55 60
 Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser
 65 70 75 80
 Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln
 85 90 95
 Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser
 100 105 110
 Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu
 115 120 125
 Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu
 130 135 140
 Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr
 145 150 155 160
 Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe
 165 170 175
 Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro
 180 185 190
 Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
 195 200 205
 Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val
 210 215 220
 Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser
 225 230 235 240
 Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr
 245 250 255
 Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly
 260 265 270
 Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg
 275 280 285

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
 290 295 300

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
 305 310 315 320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
 325 330 335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
 340 345 350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
 355 360 365

Val Val Val Pro Leu Arg Val Glx
 370 375

<210> 109
 <211> 367
 <212> PRT
 <213> Escherichia coli

<400> 109
 Met Lys Phe Thr Val Glu Arg Glu His Leu Leu Lys Pro Leu Gln Gln
 1 5 10 15

Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
 20 25 30

Leu Leu Leu Gln Val Ala Asp Gly Thr Leu Ser Leu Thr Gly Thr Asp
 35 40 45

Leu Glu Met Glu Met Val Ala Arg Val Ala Leu Val Gln Pro His Glu
 50 55 60

Pro Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Cys Arg
 65 70 75 80

Gly Leu Pro Glu Gly Ala Glu Ile Ala Val Gln Leu Glu Gly Glu Arg
 85 90 95

Met Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
 100 105 110

Ala Ala Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe

115		120		125
Thr Leu Pro Gln Ala Thr Met Lys Arg Leu Ile Glu Ala Thr Gln Phe				
130		135		140
Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe				
145		150		155
				160
Glu Thr Glu Gly Glu Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg				
		165		170
				175
Leu Ala Val Cys Ser Met Pro Ile Gly Gln Ser Leu Pro Ser His Ser				
		180		185
				190
Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Met Leu Asp				
		195		200
				205
Gly Gly Asp Asn Pro Leu Arg Val Gln Ile Gly Ser Asn Asn Ile Arg				
		210		215
				220
Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly Arg				
		225		230
				235
				240
Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Asp Lys His Leu				
		245		250
				255
Glu Ala Gly Cys Asp Leu Leu Lys Gln Ala Phe Ala Arg Ala Ala Ile				
		260		265
				270
Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Leu Tyr Val Ser Glu Asn				
		275		280
				285
Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu Glu				
		290		295
				300
Ile Leu Asp Val Thr Tyr Ser Gly Ala Glu Met Glu Ile Gly Phe Asn				
		305		310
				315
				320
Val Ser Tyr Val Leu Asp Val Leu Asn Ala Leu Lys Cys Glu Asn Val				
		325		330
				335
Arg Met Met Leu Thr Asp Ser Val Ser Ser Val Gln Ile Glu Asp Ala				
		340		345
				350
Ala Ser Gln Ser Ala Ala Tyr Val Val Met Pro Met Arg Leu Glx				
		355		360
				365

<210> 110
 <211> 367
 <212> PRT
 <213> *Proteus mirabilis*

<400> 110

Met	Lys	Phe	Ile	Ile	Glu	Arg	Glu	Gln	Leu	Leu	Lys	Pro	Leu	Gln	Gln	1	5	10	15
Val	Ser	Gly	Pro	Leu	Gly	Gly	Arg	Pro	Thr	Leu	Pro	Ile	Leu	Gly	Asn	20	25	30	
Leu	Leu	Leu	Lys	Val	Thr	Glu	Asn	Thr	Leu	Ser	Leu	Thr	Gly	Thr	Asp	35	40	45	
Leu	Glu	Met	Glu	Met	Met	Ala	Arg	Val	Ser	Leu	Ser	Gln	Ser	His	Glu	50	55	60	
Ile	Gly	Ala	Thr	Thr	Val	Pro	Ala	Arg	Lys	Phe	Phe	Asp	Ile	Trp	Arg	65	70	75	80
Gly	Leu	Pro	Glu	Gly	Ala	Glu	Ile	Ser	Val	Glu	Leu	Asp	Gly	Asp	Arg	85	90	95	
Leu	Leu	Val	Arg	Ser	Gly	Arg	Ser	Arg	Phe	Ser	Leu	Ser	Thr	Leu	Pro	100	105	110	
Ala	Ser	Asp	Phe	Pro	Asn	Leu	Asp	Asp	Trp	Gln	Ser	Glu	Val	Glu	Phe	115	120	125	
Thr	Leu	Pro	Gln	Ala	Thr	Leu	Lys	Arg	Leu	Ile	Glu	Ser	Thr	Gln	Phe	130	135	140	
Ser	Met	Ala	His	Gln	Asp	Val	Arg	Tyr	Tyr	Leu	Asn	Gly	Met	Leu	Phe	145	150	155	160
Glu	Thr	Glu	Asn	Thr	Glu	Leu	Arg	Thr	Val	Ala	Thr	Asp	Gly	His	Arg	165	170	175	
Leu	Ala	Val	Cys	Ala	Met	Asp	Ile	Gly	Gln	Ser	Leu	Pro	Gly	His	Ser	180	185	190	
Val	Ile	Val	Pro	Arg	Lys	Gly	Val	Ile	Glu	Leu	Met	Arg	Leu	Leu	Asp	195	200	205	
Gly	Ser	Gly	Glu	Ser	Leu	Leu	Gln	Leu	Gln	Ile	Gly	Ser	Asn	Asn	Leu	210	215	220	

Arg Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly
 225 230 235 240
 Arg Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Thr Lys Thr
 245 250 255
 Val Ile Ala Gly Cys Asp Ile Leu Lys Gln Ala Phe Ser Arg Ala Ala
 260 265 270
 Ile Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Ile Asn Leu Thr Asn
 275 280 285
 Gly Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu
 290 295 300
 Glu Ile Val Asp Val Gln Tyr Gln Gly Glu Glu Met Glu Ile Gly Phe
 305 310 315 320
 Asn Val Ser Tyr Leu Leu Asp Val Leu Asn Thr Leu Lys Cys Glu Glu
 325 330 335
 Val Lys Leu Leu Leu Thr Asp Ala Val Ser Ser Val Gln Val Glu Asn
 340 345 350
 Val Ala Ser Ala Ala Ala Ala Tyr Val Val Met Pro Met Arg Leu
 355 360 365

<210> 111
 <211> 366
 <212> PRT
 <213> Haemophilus influenzae

<400> 111
 Met Gln Phe Ser Ile Ser Arg Glu Asn Leu Leu Lys Pro Leu Gln Gln
 1 5 10 15
 Val Cys Gly Val Leu Ser Asn Arg Pro Asn Ile Pro Val Leu Asn Asn
 20 25 30
 Val Leu Leu Gln Ile Glu Asp Tyr Arg Leu Thr Ile Thr Gly Thr Asp
 35 40 45
 Leu Glu Val Glu Leu Ser Ser Gln Thr Gln Leu Ser Ser Ser Ser Glu
 50 55 60
 Asn Gly Thr Phe Thr Ile Pro Ala Lys Lys Phe Leu Asp Ile Cys Arg
 65 70 75 80

Thr	Leu	Ser	Asp	Asp	Ser	Glu	Ile	Thr	Val	Thr	Phe	Glu	Gln	Asp	Arg		
				85					90					95			
Ala	Leu	Val	Gln	Ser	Gly	Arg	Ser	Arg	Phe	Thr	Leu	Ala	Thr	Gln	Pro		
			100					105					110				
Ala	Glu	Glu	Tyr	Pro	Asn	Leu	Thr	Asp	Trp	Gln	Ser	Glu	Val	Asp	Phe		
			115				120					125					
Glu	Leu	Pro	Gln	Asn	Thr	Leu	Arg	Arg	Leu	Ile	Glu	Ala	Thr	Gln	Phe		
	130					135					140						
Ser	Met	Ala	Asn	Gln	Asp	Ala	Arg	Tyr	Phe	Leu	Asn	Gly	Met	Lys	Phe		
145					150					155					160		
Glu	Thr	Glu	Gly	Asn	Leu	Leu	Arg	Thr	Val	Ala	Thr	Asp	Gly	His	Arg		
				165					170					175			
Leu	Ala	Val	Cys	Thr	Ile	Ser	Leu	Glu	Gln	Glu	Leu	Gln	Asn	His	Ser		
			180					185					190				
Val	Ile	Leu	Pro	Arg	Lys	Gly	Val	Leu	Glu	Leu	Val	Arg	Leu	Leu	Glu		
			195				200					205					
Thr	Asn	Asp	Glu	Pro	Ala	Arg	Leu	Gln	Ile	Gly	Thr	Asn	Asn	Leu	Arg		
	210					215					220						
Val	His	Leu	Lys	Asn	Thr	Val	Phe	Thr	Ser	Lys	Leu	Ile	Asp	Gly	Arg		
225					230					235					240		
Phe	Pro	Asp	Tyr	Arg	Arg	Val	Leu	Pro	Arg	Asn	Ala	Thr	Lys	Ile	Val		
				245					250					255			
Glu	Gly	Asn	Trp	Glu	Met	Leu	Lys	Gln	Ala	Phe	Ala	Arg	Ala	Ser	Ile		
			260					265					270				
Leu	Ser	Asn	Glu	Arg	Ala	Arg	Ser	Val	Arg	Leu	Ser	Leu	Lys	Glu	Asn		
		275					280					285					
Gln	Leu	Lys	Ile	Thr	Ala	Ser	Asn	Thr	Glu	His	Glu	Glu	Ala	Glu	Glu		
	290					295					300						
Ile	Val	Asp	Val	Asn	Tyr	Asn	Gly	Glu	Glu	Leu	Glu	Val	Gly	Phe	Asn		
305					310					315					320		
Val	Thr	Tyr	Ile	Leu	Asp	Val	Leu	Asn	Ala	Leu	Lys	Cys	Asn	Gln	Val		
				325					330					335			

Arg Met Cys Leu Thr Asp Ala Phe Ser Ser Cys Leu Ile Glu Asn Cys
 340 345 350

Glu Asp Ser Ser Cys Glu Tyr Val Ile Met Pro Met Arg Leu
 355 360 365

<210> 112

<211> 367

<212> PRT

<213> Pseudomonas putida

<400> 112

Met His Phe Thr Ile Gln Arg Glu Ala Leu Leu Lys Pro Leu Gln Leu
 1 5 10 15

Val Ala Gly Val Val Glu Arg Arg Gln Thr Leu Pro Val Leu Ser Asn
 20 25 30

Val Leu Leu Val Val Gln Gly Gln Gln Leu Ser Leu Thr Gly Thr Asp
 35 40 45

Leu Glu Val Glu Leu Val Gly Arg Val Gln Leu Glu Glu Pro Ala Glu
 50 55 60

Pro Gly Glu Ile Thr Val Pro Ala Arg Lys Leu Met Asp Ile Cys Lys
 65 70 75 80

Ser Leu Pro Asn Asp Ala Leu Ile Asp Ile Lys Val Asp Glu Gln Lys
 85 90 95

Leu Leu Val Lys Ala Gly Arg Ser Arg Phe Thr Leu Ser Thr Leu Pro
 100 105 110

Ala Asn Asp Phe Pro Thr Val Glu Glu Gly Pro Gly Ser Leu Thr Cys
 115 120 125

Asn Leu Glu Gln Ser Lys Leu Arg Arg Leu Ile Glu Arg Thr Ser Phe
 130 135 140

Ala Met Ala Gln Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu
 145 150 155 160

Glu Val Ser Arg Asn Thr Leu Arg Ala Val Ser Thr Asp Gly His Arg
 165 170 175

Leu Ala Leu Cys Ser Met Ser Ala Pro Ile Glu Gln Glu Asp Arg His

Lys Phe Lys Val Leu Ser Asp Asn Gln Glu Glu Glu Thr Ala Glu Asp
 290 295 300

Leu Phe Glu Ile Asp Tyr Phe Gly Glu Lys Ile Glu Ile Ser Ile Asn
 305 310 315 320

Val Tyr Tyr Leu Leu Asp Val Ile Asn Asn Ile Lys Ser Glu Asn Ile
 325 330 335

Ala Leu Phe Leu Asn Lys Ser Lys Ser Ser Ile Gln Ile Glu Ala Glu
 340 345 350

Asn Asn Ser Ser Asn Ala Tyr Val Val Met Leu Leu Lys Arg
 355 360 365

<210> 114

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 114

gtgtggatcc tcgtccccct catgcgcgac caggaagg 39

<210> 115

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 115

gtgtggatcc gtggtgacct tagccac 27

<210> 116

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 116
 ttctgtgtccg aggcaccttgt ggtccacaac

30

<210> 117
 <211> 3514
 <212> DNA
 <213> Aquifex aeolicus

<400> 117
 atgagtaagg atttcgtcca ccttcacctg cacacccagt tctcactcct ggacggggct 60
 ataaagatag acgagctcgt gaaaaaggca aaggagtatg gatacaaagc tgtcggaaatg 120
 tcagaccacg gaaacctctt cggttcgtat aaattctaca aagccctgaa ggcggaagga 180
 attaaagccca taatcggcat ggaagcctac tttaccacgg gttcgagggt tgacagaaag 240
 actaaaacga gcgaggacaa cataaccgac aagtacaacc accacctcat acttatagca 300
 aaggacgaaa aggtctaaag aacttaatga agctctcaac cctcgcctac aaagaagggt 360
 tttactacaa acccagaatt gattacgaac tccttgaaaa gtacggggag ggcctaatag 420
 cccttaccgc atgcctgaaa ggtgttccca cctactacgc ttctataaac gaagtgaaaa 480
 aggcggagga atgggtaaag aagttcaagg atatatcgg agatgacctt tatttagaac 540
 ttcaagcgaa caacattcca gaacaggaag tggcaaacag gaacttaata gagatagcca 600
 aaaagtacga tgtgaaactc atagcgacgc aggcgcccc ctacctcaat cccgaagaca 660
 ggtacgcccc cacggttctt atggcacttc aaatgaaaa gaccattcac gaactgagtt 720
 cgggaaactt caagtgttca aacgaagacc ttcactttgc tccacccgag tacatgtgga 780
 aaaagtttga aggtaaagttc gaaggctggg aaaaggcact cctgaacact ctcgaggtaa 840
 tggaaaagac agcggacagc tttgagatat ttgaaaactc cacctacctc cttcccaagt 900
 acgacgttcc gcccgacaaa acccttgagg aatacctcag agaactcgcg tacaagggtt 960
 taagacagag gatagaaagg ggacaagcta aggatactaa agagtactgg gagaggctcg 1020
 agtacgaact ggaagttata aacaaaatgg gctttgctgg atacttcttg atagttcagg 1080
 acttcataaa ctgggctaag aaaaacgaca tacctgttgg acccggaagg ggaagtgtctg 1140
 gaggttccct cgtcgcatac gccatcggaa taacggacgt tgaccctata aagcacggat 1200
 tcctttttga gaggttctta aaccccgaaa gggtttccat gccggatata gacgtggatt 1260
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<210> 118

<211> 1161

<212> PRT

<213> Aquifex aeolicus

<400> 118

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Leu Asp Gly Ala Ile Lys Ile Asp Glu Leu Val Lys Lys Ala Lys Glu
      20              25              30

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Tyr Gly Tyr Lys Ala Val Gly Met Ser Asp His Gly Asn Leu Phe Gly
    35              40              45

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```

Ser Tyr Lys Phe Tyr Lys Ala Leu Lys Ala Glu Gly Ile Lys Pro Ile
    50              55              60

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Ile Gly Met Glu Ala Tyr Phe Thr Thr Gly Ser Arg Phe Asp Arg Lys
    65              70              75              80

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Thr Lys Thr Ser Glu Asp Asn Ile Thr Asp Lys Tyr Asn His His Leu
      85              90              95

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Ile Leu Ile Ala Lys Asp Asp Lys Gly Leu Lys Asn Leu Met Lys Leu

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100					105					110						
Ser	Thr	Leu	Ala	Tyr	Lys	Glu	Gly	Phe	Tyr	Tyr	Lys	Pro	Arg	Ile	Asp	
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Tyr	Glu	Leu	Leu	Glu	Lys	Tyr	Gly	Glu	Gly	Leu	Ile	Ala	Leu	Thr	Ala	
130					135					140						
Cys	Leu	Lys	Gly	Val	Pro	Thr	Tyr	Tyr	Ala	Ser	Ile	Asn	Glu	Val	Lys	
145					150					155					160	
Lys	Ala	Glu	Glu	Trp	Val	Lys	Lys	Phe	Lys	Asp	Ile	Phe	Gly	Asp	Asp	
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Leu	Tyr	Leu	Glu	Leu	Gln	Ala	Asn	Asn	Ile	Pro	Glu	Gln	Glu	Val	Ala	
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Asn	Arg	Asn	Leu	Ile	Glu	Ile	Ala	Lys	Lys	Tyr	Asp	Val	Lys	Leu	Ile	
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Thr	Val	Leu	Met	Ala	Leu	Gln	Met	Lys	Lys	Thr	Ile	His	Glu	Leu	Ser	
225					230					235					240	
Ser	Gly	Asn	Phe	Lys	Cys	Ser	Asn	Glu	Asp	Leu	His	Phe	Ala	Pro	Pro	
245					250					255						
Glu	Tyr	Met	Trp	Lys	Lys	Phe	Glu	Gly	Lys	Phe	Glu	Gly	Trp	Glu	Lys	
260					265					270						
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Glu	Ile	Phe	Glu	Asn	Ser	Thr	Tyr	Leu	Leu	Pro	Lys	Tyr	Asp	Val	Pro	
290					295					300						
Pro	Asp	Lys	Thr	Leu	Glu	Glu	Tyr	Leu	Arg	Glu	Leu	Ala	Tyr	Lys	Gly	
305					310					315					320	
Leu	Arg	Gln	Arg	Ile	Glu	Arg	Gly	Gln	Ala	Lys	Asp	Thr	Lys	Glu	Tyr	
325					330					335						
Trp	Glu	Arg	Leu	Glu	Tyr	Glu	Leu	Glu	Val	Ile	Asn	Lys	Met	Gly	Phe	
340					345					350						
Ala	Gly	Tyr	Phe	Leu	Ile	Val	Gln	Asp	Phe	Ile	Asn	Trp	Ala	Lys	Lys	

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625	630	635 640
Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu Leu Leu Lys Lys Leu		
	645	650 655
Lys Pro Asp Ser Phe Asp Asp Ile Val Ala Val Leu Ala Leu Tyr Arg		
	660	665 670
Pro Gly Pro Leu Lys Ser Gly Leu Val Asp Thr Tyr Ile Lys Arg Lys		
	675	680 685
His Gly Lys Glu Pro Val Glu Tyr Pro Phe Pro Glu Leu Glu Pro Val		
	690	695 700
Leu Lys Glu Thr Tyr Gly Val Ile Val Tyr Gln Glu Gln Val Met Lys		
	705	710 715 720
Met Ser Gln Ile Leu Ser Gly Phe Thr Pro Gly Glu Ala Asp Thr Leu		
	725	730 735
Arg Lys Ala Ile Gly Lys Lys Lys Ala Asp Leu Met Ala Gln Met Lys		
	740	745 750
Asp Lys Phe Ile Gln Gly Ala Val Glu Arg Gly Tyr Pro Glu Glu Lys		
	755	760 765
Ile Arg Lys Leu Trp Glu Asp Ile Glu Lys Phe Ala Ser Tyr Ser Phe		
	770	775 780
Asn Lys Ser His Ser Val Ala Tyr Gly Tyr Ile Ser Tyr Trp Thr Ala		
	785	790 795 800
Tyr Val Lys Ala His Tyr Pro Ala Glu Phe Phe Ala Val Lys Leu Thr		
	805	810 815
Thr Glu Lys Asn Asp Asn Lys Phe Leu Asn Leu Ile Lys Asp Ala Lys		
	820	825 830
Leu Phe Gly Phe Glu Ile Leu Pro Pro Asp Ile Asn Lys Ser Asp Val		
	835	840 845
Gly Phe Thr Ile Glu Gly Glu Asn Arg Ile Arg Phe Gly Leu Ala Arg		
	850	855 860
Ile Lys Gly Val Gly Glu Glu Thr Ala Lys Ile Ile Val Glu Ala Arg		

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	885		890		895	
Lys Asn Arg Lys Ile Asn Lys Lys Val Val Glu Ala Leu Val Lys Ala						
	900		905		910	
Gly Ala Phe Asp Phe Thr Lys Lys Lys Arg Lys Glu Leu Leu Ala Lys						
	915		920		925	
Val Ala Asn Ser Glu Lys Ala Leu Met Ala Thr Gln Asn Ser Leu Phe						
	930		935		940	
Gly Ala Pro Lys Glu Glu Val Glu Glu Leu Asp Pro Leu Lys Leu Glu						
945		950		955		960
Lys Glu Val Leu Gly Phe Tyr Ile Ser Gly His Pro Leu Asp Asn Tyr						
	965		970		975	
Glu Lys Leu Leu Lys Asn Arg Tyr Thr Pro Ile Glu Asp Leu Glu Glu						
	980		985		990	
Trp Asp Lys Glu Ser Glu Ala Val Leu Thr Gly Val Ile Thr Glu Leu						
	995		1000		1005	
Lys Val Lys Lys Thr Lys Asn Gly Asp Tyr Met Ala Val Phe Asn Leu						
1010		1015		1020		
Val Asp Lys Thr Gly Leu Ile Glu Cys Val Val Phe Pro Gly Val Tyr						
1025		1030		1035		1040
Glu Glu Ala Lys Glu Leu Ile Glu Glu Asp Arg Val Val Val Val Lys						
	1045		1050		1055	
Gly Phe Leu Asp Glu Asp Leu Glu Thr Glu Asn Val Lys Phe Val Val						
	1060		1065		1070	
Lys Glu Val Phe Ser Pro Glu Glu Phe Ala Lys Glu Met Arg Asn Thr						
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Leu Tyr Ile Phe Leu Lys Arg Glu Gln Ala Leu Asn Gly Val Ala Glu						
	1090		1095		1100	
Lys Leu Lys Gly Ile Ile Glu Asn Asn Arg Thr Glu Asp Gly Tyr Asn						
1105		1110		1115		1120
Leu Val Leu Thr Val Asp Leu Gly Asp Tyr Phe Val Asp Leu Ala Leu						

1125	1130	1135
Pro Gln Asp Met Lys Leu Lys Ala Asp Arg Lys Val Val Glu Glu Ile		
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Glu Lys Leu Gly Val Lys Val Ile Ile		
1155	1160	

<210> 119
 <211> 2408
 <212> DNA
 <213> Aquifex aeolicus

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<210> 120
<211> 473
<212> PRT
<213> Aquifex aeolicus

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Glu Val Ile Gly Gln Glu Ala Pro Val Arg Ile Leu Lys Asn Ala Ile
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Lys Asn Asp Arg Val Ala His Ala Tyr Leu Phe Ala Gly Pro Arg Gly
      35             40            45

Val Gly Lys Thr Thr Ile Ala Arg Ile Leu Ala Lys Ala Leu Asn Cys
      50             55            60

Lys Asn Pro Ser Lys Gly Glu Pro Cys Gly Glu Cys Glu Asn Cys Arg
      65             70            75            80

Glu Ile Asp Arg Gly Val Phe Pro Asp Leu Ile Glu Met Asp Ala Ala
      85             90            95

Ser Asn Arg Gly Ile Asp Asp Val Arg Ala Leu Lys Glu Ala Val Asn
      100            105            110

Tyr Lys Pro Ile Lys Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Ala
      115            120            125

His Met Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
      130            135            140

Glu Pro Pro Pro Arg Thr Val Phe Val Leu Cys Thr Thr Glu Tyr Asp
      145            150            155            160

Lys Ile Leu Pro Thr Ile Leu Ser Arg Cys Gln Arg Ile Ile Phe Ser
      165            170            175

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Lys	Val	Arg	Lys	Glu	Lys	Val	Ile	Glu	Tyr	Leu	Lys	Lys	Ile	Cys	Glu	180	185	190
Lys	Glu	Gly	Ile	Glu	Cys	Glu	Glu	Gly	Ala	Leu	Glu	Val	Leu	Ala	His	195	200	205
Ala	Ser	Glu	Gly	Cys	Met	Arg	Asp	Ala	Ala	Ser	Leu	Leu	Asp	Gln	Ala	210	215	220
Ser	Val	Tyr	Gly	Glu	Gly	Arg	Val	Thr	Lys	Glu	Val	Val	Glu	Asn	Phe	225	230	235
Leu	Gly	Ile	Leu	Ser	Gln	Glu	Ser	Val	Arg	Ser	Phe	Leu	Lys	Leu	Leu	245	250	255
Leu	Asn	Ser	Glu	Val	Asp	Glu	Ala	Ile	Lys	Phe	Leu	Arg	Glu	Leu	Ser	260	265	270
Glu	Lys	Gly	Tyr	Asn	Leu	Thr	Lys	Phe	Trp	Glu	Met	Leu	Glu	Glu	Glu	275	280	285
Val	Arg	Asn	Ala	Ile	Leu	Val	Lys	Ser	Leu	Lys	Asn	Pro	Glu	Ser	Val	290	295	300
Val	Gln	Asn	Trp	Gln	Asp	Tyr	Glu	Asp	Phe	Lys	Asp	Tyr	Pro	Leu	Glu	305	310	315
Ala	Leu	Leu	Tyr	Val	Glu	Asn	Leu	Ile	Asn	Arg	Gly	Lys	Val	Glu	Ala	325	330	335
Arg	Thr	Arg	Glu	Pro	Leu	Arg	Ala	Phe	Glu	Leu	Ala	Val	Ile	Lys	Ser	340	345	350
Leu	Ile	Val	Lys	Asp	Ile	Ile	Pro	Val	Ser	Gln	Leu	Gly	Ser	Val	Val	355	360	365
Lys	Glu	Thr	Lys	Lys	Glu	Glu	Lys	Lys	Val	Glu	Val	Lys	Glu	Glu	Pro	370	375	380
Lys	Val	Lys	Glu	Glu	Lys	Pro	Lys	Glu	Gln	Glu	Glu	Asp	Arg	Phe	Gln	385	390	395
Lys	Val	Leu	Asn	Ala	Val	Asp	Gly	Lys	Ile	Leu	Lys	Arg	Ile	Leu	Glu	405	410	415
Gly	Ala	Lys	Arg	Glu	Glu	Arg	Asp	Gly	Lys	Ile	Val	Leu	Lys	Ile	Glu	420	425	430

Ala Ser Tyr Leu Arg Thr Met Lys Lys Glu Phe Asp Ser Leu Lys Glu
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Thr Phe Pro Phe Leu Glu Phe Glu Pro Val Glu Asp Lys Lys Lys Pro
 450 455 460

Gln Lys Ser Ser Gly Thr Arg Leu Phe
 465 470

<210> 121
 <211> 1090
 <212> DNA
 <213> Aquifex aeolicus

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 aacttaatcg taagggaac ggacttgga aactaccttg tagtctccgt aaagggggag 180
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 aagagtacgt acaaacttcc gacagctccc gcggaggact ttcccgaatt tccagaaatc 360
 gtagaaggag gagaaacact ttcgggaaac cttctcgtta acggaataga aaaggtagag 420
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 ccaagtcttc 1090

<210> 122
 <211> 363
 <212> PRT
 <213> Aquifex aeolicus

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Ala Arg Glu Ser Thr Glu Lys Lys Ala Ala Leu Pro Ile Leu Ala Asn

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Phe	Leu	Leu	Ser	Ala	Lys	Glu	Glu	Asn	Leu	Ile	Val	Arg	Ala	Thr	Asp
	35					40						45			
Leu	Glu	Asn	Tyr	Leu	Val	Val	Ser	Val	Lys	Gly	Glu	Val	Glu	Glu	Glu
	50					55					60				
Gly	Glu	Val	Cys	Val	His	Ser	Gln	Lys	Leu	Tyr	Asp	Ile	Val	Lys	Asn
	65				70					75					80
Leu	Asn	Ser	Ala	Tyr	Val	Tyr	Leu	His	Thr	Glu	Gly	Glu	Lys	Leu	Val
				85					90					95	
Ile	Thr	Gly	Gly	Lys	Ser	Thr	Tyr	Lys	Leu	Pro	Thr	Ala	Pro	Ala	Glu
		100						105						110	
Asp	Phe	Pro	Glu	Phe	Pro	Glu	Ile	Val	Glu	Gly	Gly	Glu	Thr	Leu	Ser
		115					120					125			
Gly	Asn	Leu	Leu	Val	Asn	Gly	Ile	Glu	Lys	Val	Glu	Tyr	Ala	Ile	Ala
	130					135					140				
Lys	Glu	Glu	Ala	Asn	Ile	Ala	Leu	Gln	Gly	Met	Tyr	Leu	Arg	Gly	Tyr
	145				150					155					160
Glu	Asp	Arg	Ile	His	Phe	Val	Gly	Ser	Asp	Gly	His	Arg	Leu	Ala	Leu
			165						170					175	
Tyr	Glu	Pro	Leu	Gly	Glu	Phe	Ser	Lys	Glu	Leu	Leu	Ile	Pro	Arg	Lys
		180						185						190	
Ser	Leu	Lys	Val	Leu	Lys	Lys	Leu	Ile	Thr	Gly	Ile	Glu	Asp	Val	Asn
		195					200					205			
Ile	Glu	Lys	Ser	Glu	Asp	Glu	Ser	Phe	Ala	Tyr	Phe	Ser	Thr	Pro	Glu
	210					215					220				
Trp	Lys	Leu	Ala	Val	Arg	Leu	Leu	Glu	Gly	Glu	Phe	Pro	Asp	Tyr	Met
	225				230					235					240
Ser	Val	Ile	Pro	Glu	Glu	Phe	Ser	Ala	Glu	Val	Leu	Phe	Glu	Thr	Glu
				245					250					255	
Glu	Val	Leu	Lys	Val	Leu	Lys	Arg	Leu	Lys	Ala	Leu	Ser	Glu	Gly	Lys
		260					265						270		
Val	Phe	Pro	Val	Lys	Ile	Thr	Leu	Ser	Glu	Asn	Leu	Ala	Ile	Phe	Glu

275	280	285
Phe Ala Asp Pro Glu Phe Gly Glu Ala Arg Glu Glu Ile Glu Val Glu		
290	295	300
Tyr Thr Gly Glu Pro Phe Glu Ile Gly Phe Asn Gly Lys Tyr Leu Met		
305	310	315
Glu Ala Leu Asp Ala Tyr Asp Ser Glu Arg Val Trp Phe Lys Phe Thr		
325	330	335
Thr Pro Asp Thr Ala Thr Leu Leu Glu Ala Glu Asp Tyr Glu Lys Glu		
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Pro Tyr Lys Cys Ile Ile Met Pro Met Arg Val		
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<210> 123
 <211> 1093
 <212> DNA
 <213> Aquifex aeolicus

<400> 123

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gaaaagtacg	gggagaatta	cacggttctg	tgggggggatg	agataagcga	ggaggaattc	180
tacactgccc	tttccgagac	cagtatattc	ggcggttcaa	aggaaaaagc	ggtggtcatt	240
tacaacttcg	gggatttcct	gaagaagctc	ggaaggaaga	aaaaggaaaa	agaaaggctt	300
ataaaagtcc	tcagaaacgt	aaagagtaac	tacgtattta	tagtgtacga	tgcgaaactc	360
cagaaacagg	aactttcttc	ggaacctctg	aaatccgtag	cgtctttcgg	cggtatagtg	420
gtagcaacaa	ggctgagcaa	ggagaggata	aaacagctcg	tccttaagaa	gttcaaagaa	480
aaagggataa	acgtagaaaa	cgatgccctt	gaataccttc	tccagctcac	gggttacaac	540
ttgatggagc	tcaaacttga	ggttgaaaaa	ctgatagatt	acgcaagtga	aaagaaaatt	600
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gagttcgttg	atttactcct	cttaaaagat	tacgaaaagg	ctcttaaagt	tttggactcc	720
ctcatttcct	tcggaataca	ccccctccag	attatgaaaa	tcctgtcctc	ctatgctcta	780
aaactttaca	ccctcaagag	gcttgaagag	aaggaggagg	acctgaataa	ggcgatggaa	840
agcgtgggaa	taaagaacaa	ctttctcaag	atgaagttca	aatcttactt	aaaggcaaac	900
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ctttactttc	aggacacagt	gcagttgctg	gggatttctt	gacctcaaga	ctggagaggg	1020
aagttgtgaa	aaatacttct	catggtggat	aatctttttt	atgaagtttg	cggtttgcgt	1080
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<210> 124
 <211> 350
 <212> PRT

<213> Aquifex aeolicus

<400> 124

Val	Glu	Thr	Thr	Ile	Phe	Gln	Phe	Gln	Lys	Thr	Phe	Phe	Thr	Lys	Pro	
1				5					10					15		
Pro	Lys	Glu	Arg	Val	Phe	Val	Leu	His	Gly	Glu	Glu	Gln	Tyr	Leu	Ile	
			20					25					30			
Arg	Thr	Phe	Leu	Ser	Lys	Leu	Lys	Glu	Lys	Tyr	Gly	Glu	Asn	Tyr	Thr	
		35					40					45				
Val	Leu	Trp	Gly	Asp	Glu	Ile	Ser	Glu	Glu	Glu	Phe	Tyr	Thr	Ala	Leu	
	50					55					60					
Ser	Glu	Thr	Ser	Ile	Phe	Gly	Gly	Ser	Lys	Glu	Lys	Ala	Val	Val	Ile	
65				70						75					80	
Tyr	Asn	Phe	Gly	Asp	Phe	Leu	Lys	Lys	Leu	Gly	Arg	Lys	Lys	Lys	Glu	
			85						90						95	
Lys	Glu	Arg	Leu	Ile	Lys	Val	Leu	Arg	Asn	Val	Lys	Ser	Asn	Tyr	Val	
			100					105					110			
Phe	Ile	Val	Tyr	Asp	Ala	Lys	Leu	Gln	Lys	Gln	Glu	Leu	Ser	Ser	Glu	
		115					120					125				
Pro	Leu	Lys	Ser	Val	Ala	Ser	Phe	Gly	Gly	Ile	Val	Val	Ala	Asn	Arg	
	130					135					140					
Leu	Ser	Lys	Glu	Arg	Ile	Lys	Gln	Leu	Val	Leu	Lys	Lys	Phe	Lys	Glu	
145				150					155						160	
Lys	Gly	Ile	Asn	Val	Glu	Asn	Asp	Ala	Leu	Glu	Tyr	Leu	Leu	Gln	Leu	
			165						170					175		
Thr	Gly	Tyr	Asn	Leu	Met	Glu	Leu	Lys	Leu	Glu	Val	Glu	Lys	Leu	Ile	
		180						185					190			
Asp	Tyr	Ala	Ser	Glu	Lys	Lys	Ile	Leu	Thr	Leu	Asp	Glu	Val	Lys	Arg	
		195					200					205				
Val	Ala	Phe	Ser	Val	Ser	Glu	Asn	Val	Asn	Val	Phe	Glu	Phe	Val	Asp	
	210					215					220					
Leu	Leu	Leu	Leu	Lys	Asp	Tyr	Glu	Lys	Ala	Leu	Lys	Val	Leu	Asp	Ser	
225				230						235					240	

Leu Ile Ser Phe Gly Ile His Pro Leu Gln Ile Met Lys Ile Leu Ser
245 250 255

Ser Tyr Ala Leu Lys Leu Tyr Thr Leu Lys Arg Leu Glu Glu Lys Gly
260 265 270

Glu Asp Leu Asn Lys Ala Met Glu Ser Val Gly Ile Lys Asn Asn Phe
275 280 285

Leu Lys Met Lys Phe Lys Ser Tyr Leu Lys Ala Asn Ser Lys Glu Asp
290 295 300

Leu Lys Asn Leu Ile Leu Ser Leu Gln Arg Ile Asp Ala Phe Ser Lys
305 310 315 320

Leu Tyr Phe Gln Asp Thr Val Gln Leu Leu Arg Asp Phe Leu Thr Ser
325 330 335

Arg Leu Glu Arg Glu Val Val Lys Asn Thr Ser His Gly Gly
340 345 350

<210> 125

<211> 1051

<212> DNA

<213> Aquifex aeolicus

<400> 125

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ttatgtaagg aaaacgtacc tggggatgcg gaagttgtcc ctctgcaaa cacgtaaacg 180
agctggagga agccttcttt aaaggagaaa tagaagactt taaagtttat aagacaagga 240
cggtaaaaag cacttcgttt accttatggg cgaacatccc gactttgttg taataatccc 300
gagcggacat tacataaaga tagaacagat aagggaagtt aagaactttg cctatgtgaa 360
gcccgcacta agcaggagaa aagtaattat aatagacgac gccacgcga tgacctctca 420
ggcggcaaac gctcttttaa aggtattgga agagccacct gcggacacca cttttatctt 480
gaccacgaac aggcgttctg caatcctgcc gactatcctc tccagaactt ttcaagtgga 540
gttcaagggc ttttcagtaa aagaggttat ggaaatagcg aaagtagacg aggaaatagc 600
gaaactctct ggaggcagtc taaaaagggc tatcttacta aaggaaaaca aagatattct 660
aaacaaagta aaggaattct tggaaaacga gccgttaaaa gtttacaagc ttgcaagtga 720
attcgaaaag tgggaacctg aaaagcaaaa actcttcctt gaaattatgg aagaattggt 780
atctcaaaaa ttgaccgaag agaaaaaaga caattacacc taccttcttg atacgatcag 840
actctttaa gacggactcg caaggggtgt aaacgaacct ctgtggctgt ttacgttagc 900
cgttcaggcg gattaataaa ccgttattga ttccgtaaca tttaaacctt aatctaaatt 960
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ggaagatagg aaccgtgagc ggtgtaaaa g t 1051

```

<210> 126
 <211> 305
 <212> PRT
 <213> Aquifex aeolicus

<400> 126

Met	Glu	Lys	Val	Phe	Leu	Glu	Lys	Leu	Gln	Lys	Thr	Leu	His	Ile	Pro
1				5					10					15	
Gly	Gly	Leu	Leu	Phe	Tyr	Gly	Lys	Glu	Gly	Ser	Gly	Lys	Thr	Lys	Thr
			20					25					30		
Ala	Phe	Glu	Phe	Ala	Lys	Gly	Ile	Leu	Cys	Lys	Glu	Asn	Val	Pro	Trp
		35					40					45			
Gly	Cys	Gly	Ser	Cys	Pro	Ser	Cys	Lys	His	Val	Asn	Glu	Leu	Glu	Glu
	50					55					60				
Ala	Phe	Phe	Lys	Gly	Glu	Ile	Glu	Asp	Phe	Lys	Val	Tyr	Lys	Asp	Lys
65					70					75					80
Asp	Gly	Lys	Lys	His	Phe	Val	Tyr	Leu	Met	Gly	Glu	His	Pro	Asp	Phe
				85					90					95	
Val	Val	Ile	Ile	Pro	Ser	Gly	His	Tyr	Ile	Lys	Ile	Glu	Gln	Ile	Arg
			100					105					110		
Glu	Val	Lys	Asn	Phe	Ala	Tyr	Val	Lys	Pro	Ala	Leu	Ser	Arg	Arg	Lys
		115					120					125			
Val	Ile	Ile	Ile	Asp	Asp	Ala	His	Ala	Met	Thr	Ser	Gln	Ala	Ala	Asn
	130					135					140				
Ala	Leu	Leu	Lys	Val	Leu	Glu	Glu	Pro	Pro	Ala	Asp	Thr	Thr	Phe	Ile
145					150					155					160
Leu	Thr	Thr	Asn	Arg	Arg	Ser	Ala	Ile	Leu	Pro	Thr	Ile	Leu	Ser	Arg
			165						170					175	
Thr	Phe	Gln	Val	Glu	Phe	Lys	Gly	Phe	Ser	Val	Lys	Glu	Val	Met	Glu
			180					185					190		
Ile	Ala	Lys	Val	Asp	Glu	Glu	Ile	Ala	Lys	Leu	Ser	Gly	Gly	Ser	Leu
		195					200					205			
Lys	Arg	Ala	Ile	Leu	Leu	Lys	Glu	Asn	Lys	Asp	Ile	Leu	Asn	Lys	Val
	210					215					220				

Lys Glu Phe Leu Glu Asn Glu Pro Leu Lys Val Tyr Lys Leu Ala Ser
 225 230 235 240

Glu Phe Glu Lys Trp Glu Pro Glu Lys Gln Lys Leu Phe Leu Glu Ile
 245 250 255

Met Glu Glu Leu Val Ser Gln Lys Leu Thr Glu Glu Lys Lys Asp Asn
 260 265 270

Tyr Thr Tyr Leu Leu Asp Thr Ile Arg Leu Phe Lys Asp Gly Leu Ala
 275 280 285

Arg Gly Val Asn Glu Pro Leu Trp Leu Phe Thr Leu Ala Val Gln Ala
 290 295 300

Asp
 305

<210> 127
 <211> 630
 <212> DNA
 <213> Aquifex aeolicus

<400> 127
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 gagttctacg aagaaatcga tttgaaccag aaggtgaaag atgcaagggt tgtagttttt 120
 gactgcgaag ccacagaact cgacgtaaag aaggcaaaac tcctttcaat aggtgcgggt 180
 gaggttaaaa acctggaaat agacctctct aaatcttttt acgagatact caaaagtgac 240
 gagataaagg cggcggagat acatggaata accagggaag acgttgaaaa gtacggaaag 300
 gaaccaaagg aagtaatata cgactttctg aagtacataa agggaagcgt tctcgttggc 360
 tactacgtga agtttgacgt ctcaactcgt gagaagtact ccataaagta cttccagtat 420
 ccaatcatca actacaagtt agacctgttt agtttcgtga agagagagta ccagagtggc 480
 aggagtcttg acgaccttat gaaggaactc ggtgtagaaa taagggcaag gcacaacgcc 540
 cttgaagatg cctacataac cgctcttctt ttcctaaagt acgtttaccc gaacagggag 600
 tacagactaa aggatctccc gattttcctt 630

<210> 128
 <211> 210
 <212> PRT
 <213> Aquifex aeolicus

<400> 128
 Met Asn Phe Leu Lys Lys Phe Leu Leu Leu Arg Lys Ala Gln Lys Ser
 1 5 10 15
 Pro Tyr Phe Glu Glu Phe Tyr Glu Glu Ile Asp Leu Asn Gln Lys Val

20	25	30
Lys Asp Ala Arg Phe Val Val Phe Asp Cys Glu Ala Thr Glu Leu Asp		
35	40	45
Val Lys Lys Ala Lys Leu Leu Ser Ile Gly Ala Val Glu Val Lys Asn		
50	55	60
Leu Glu Ile Asp Leu Ser Lys Ser Phe Tyr Glu Ile Leu Lys Ser Asp		
65	70	75
Glu Ile Lys Ala Ala Glu Ile His Gly Ile Thr Arg Glu Asp Val Glu		
85	90	95
Lys Tyr Gly Lys Glu Pro Lys Glu Val Ile Tyr Asp Phe Leu Lys Tyr		
100	105	110
Ile Lys Gly Ser Val Leu Val Gly Tyr Tyr Val Lys Phe Asp Val Ser		
115	120	125
Leu Val Glu Lys Tyr Ser Ile Lys Tyr Phe Gln Tyr Pro Ile Ile Asn		
130	135	140
Tyr Lys Leu Asp Leu Phe Ser Phe Val Lys Arg Glu Tyr Gln Ser Gly		
145	150	155
Arg Ser Leu Asp Asp Leu Met Lys Glu Leu Gly Val Glu Ile Arg Ala		
165	170	175
Arg His Asn Ala Leu Glu Asp Ala Tyr Ile Thr Ala Leu Leu Phe Leu		
180	185	190
Lys Tyr Val Tyr Pro Asn Arg Glu Tyr Arg Leu Lys Asp Leu Pro Ile		
195	200	205
Phe Leu		
210		

<210> 129

<211> 526

<212> DNA

<213> Aquifex aeolicus

<400> 129

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 ccgagcggaa cgcccgtagt agagtttact ctggcttaca acagaaggta taaaaaccag 120
 aacggtgaat ttcaggagga aagtcacttc tttgacgtaa aggcgtacgg aaaaatggct 180

```

gaagactggg ctacacgctt ctcgaaagga tacctcgtac tcgtagaggg aagactctcc 240
caggaaaagt gggagaaaga aggaaagaag ttctcaaagg tcaggataat agcggaaaac 300
gtaagattaa taaacaggcc gaaaggtgct gaacttcaag cagaagaaga ggaggaagtt 360
cctcccattg aggaggaaat tgaaaaactc ggtaaagagg aagagaagcc ttttaccgat 420
gaagaggacg aaataccttt ttaattttga ggagggtaaa gtatggtagt gagagctcct 480
aagaagaaag tttgtatgta ctgtgaacaa aagagagagc cagatt 526

```

<210> 130

<211> 147

<212> PRT

<213> Aquifex aeolicus

<400> 130

```

Met Leu Asn Lys Val Phe Ile Ile Gly Arg Leu Thr Gly Asp Pro Val
  1             5             10             15

```

```

Ile Thr Tyr Leu Pro Ser Gly Thr Pro Val Val Glu Phe Thr Leu Ala
      20             25             30

```

```

Tyr Asn Arg Arg Tyr Lys Asn Gln Asn Gly Glu Phe Gln Glu Glu Ser
      35             40             45

```

```

His Phe Phe Asp Val Lys Ala Tyr Gly Lys Met Ala Glu Asp Trp Ala
      50             55             60

```

```

Thr Arg Phe Ser Lys Gly Tyr Leu Val Leu Val Glu Gly Arg Leu Ser
      65             70             75             80

```

```

Gln Glu Lys Trp Glu Lys Glu Gly Lys Lys Phe Ser Lys Val Arg Ile
      85             90             95

```

```

Ile Ala Glu Asn Val Arg Leu Ile Asn Arg Pro Lys Gly Ala Glu Leu
      100            105            110

```

```

Gln Ala Glu Glu Glu Glu Glu Val Pro Pro Ile Glu Glu Glu Ile Glu
      115            120            125

```

```

Lys Leu Gly Lys Glu Glu Glu Lys Pro Phe Thr Asp Glu Glu Asp Glu
      130            135            140

```

```

Ile Pro Phe
145

```

<210> 131

<211> 1472

<212> DNA

<213> Aquifex aeolicus

<400> 131

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atgcttgaag accccgaaaa catacctctg gtacttgaat accttaaaga agaagacttc 120
tgcatagacg agcacaagct acttttcagg gttcttataa acctctgggtc cgagtacggc 180
aataagctcg atttcgtatt aataaaggat caccttgaaa agaaaaactt actccagaaa 240
atacctatag actggctcga agaactctac gaggaggcgg tatcccctga cacgcttgag 300
gaagtctgca aaatagtaaa acaacgttcc gcacagaggg cgataattca actcgggtata 360
gaactcattc acaaaggaaa ggaaaacaaa gactttcaca cattaatcga ggaagcccag 420
agcaggatat tttccatagc ggaaagtgtc acatctacgc agttttacca tgtgaaagac 480
gttgcggaag aagttataga actcatttat aaattcaaaa gctctgacag gctagtcacg 540
ggactcccaa gcggtttcac ggaactcgat ctaaagacga cgggattcca ccctggagac 600
ttaataatac tcgccgcaag acccggtatg gggaaaaccg cctttatgct ctccataatc 660
tacaatctcg caaaagacga gggaaaaccc tcagctgtat tttccttgga aatgagcaag 720
gaacagctcg ttatgagact cctctctatg atgtcggagg tcccactttt caagataagg 780
tctggaagta tatcgaatga agatttaaag aagcttgaag caagcgcaat agaactcgca 840
aagtacgaca tatacctcga cgacacaccc gctctcacta caacggattt aaggataagg 900
gcaagaaagc tcagaaagga aaaggaagtt gagttcgtgg cggtggacta cttgcaactt 960
ctgagaccgc cagtccgaaa gagttcaaga caggaggaag tggcagaggt ttcaagaaac 1020
ttaaaagccc ttgcaaagga acttcacatt cccgttatgg cacttgcgca gctctcccg 1080
gaggtggaag agaggagtga taaaagaccc cagcttgcgg acctcagaga atccggacag 1140
atagaacagg acgcagacct aatccttttc ctccacagac ccgagtacta caagaaaaag 1200
ccaaatcccg aagagcaggg tatagcggaa gtgataatag ccaagcaaag gcaaggaccc 1260
acggacattg tgaagctcgc atttattaag gactacacta agtttgcaaa cctagaagcc 1320
cttcctgaac aacctcctga agaagaggaa ctttccgaaa ttattgaaac acaggaggat 1380
gaaggattcg aagatattga cttctgaaaa ttaaggtttt ataattttat cttggctatc 1440
cggggtagct caatcggcag agcgggtggc tg 1472
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<210> 132

<211> 438

<212> PRT

<213> Aquifex aeolicus

<400> 132

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Met Gln Phe Val Asp Lys Leu Pro Cys Asp Glu Ser Ala Glu Arg Ala
  1             5             10             15
```

```
Val Leu Gly Ser Met Leu Glu Asp Pro Glu Asn Ile Pro Leu Val Leu
      20             25             30
```

```
Glu Tyr Leu Lys Glu Glu Asp Phe Cys Ile Asp Glu His Lys Leu Leu
      35             40             45
```

```
Phe Arg Val Leu Thr Asn Leu Trp Ser Glu Tyr Gly Asn Lys Leu Asp
      50             55             60
```

Phe Val Leu Ile Lys Asp His Leu Glu Lys Lys Asn Leu Leu Gln Lys
 65 70 75 80
 Ile Pro Ile Asp Trp Leu Glu Glu Leu Tyr Glu Glu Ala Val Ser Pro
 85 90 95
 Asp Thr Leu Glu Glu Val Cys Lys Ile Val Lys Gln Arg Ser Ala Gln
 100 105 110
 Arg Ala Ile Ile Gln Leu Gly Ile Thr Ser Thr Gln Phe Tyr His Val
 115 120 125
 Lys Asp Val Ala Glu Glu Val Ile Glu Leu Ile Tyr Lys Phe Lys Ser
 130 135 140
 Ser Asp Arg Leu Val Thr Gly Leu Pro Ser Gly Phe Thr Glu Leu Asp
 145 150 155 160
 Leu Lys Thr Thr Gly Phe His Pro Gly Asp Leu Ile Ile Leu Ala Ala
 165 170 175
 Arg Pro Gly Met Gly Lys Thr Ala Phe Met Leu Ser Ile Ile Tyr Asn
 180 185 190
 Leu Ala Lys Asp Glu Gly Lys Pro Ser Ala Val Phe Ser Leu Glu Met
 195 200 205
 Ser Lys Glu Gln Leu Val Met Arg Leu Leu Ser Met Met Ser Glu Val
 210 215 220
 Pro Leu Phe Lys Ile Arg Ser Gly Ser Ile Ser Asn Glu Asp Leu Lys
 225 230 235 240
 Lys Leu Glu Ala Ser Ala Ile Glu Leu Ala Lys Tyr Asp Ile Tyr Leu
 245 250 255
 Asp Asp Thr Pro Ala Leu Thr Thr Thr Asp Leu Arg Ile Arg Ala Arg
 260 265 270
 Lys Leu Arg Lys Glu Lys Glu Val Glu Phe Val Ala Val Asp Tyr Leu
 275 280 285
 Gln Leu Leu Arg Pro Pro Val Arg Lys Ser Ser Arg Gln Glu Glu Val
 290 295 300
 Ala Glu Val Ser Arg Asn Leu Lys Ala Leu Ala Lys Glu Leu His Ile
 305 310 315 320

Pro Val Met Ala Leu Ala Gln Leu Ser Arg Glu Val Glu Lys Arg Ser
325 330 335

Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu Ser Gly Gln Ile Glu
340 345 350

Gln Asp Ala Asp Leu Ile Leu Phe Leu His Arg Pro Glu Tyr Tyr Lys
355 360 365

Lys Lys Pro Asn Pro Glu Glu Gln Gly Ile Ala Glu Val Ile Ile Ala
370 375 380

Lys Gln Arg Gln Gly Pro Thr Asp Ile Val Lys Leu Ala Phe Ile Lys
385 390 395 400

Glu Tyr Thr Lys Phe Ala Asn Leu Glu Ala Leu Pro Glu Gln Pro Pro
405 410 415

Glu Glu Glu Glu Leu Ser Glu Ile Ile Glu Thr Gln Glu Asp Glu Gly
420 425 430

Phe Glu Asp Ile Asp Phe
435

<210> 133

<211> 1526

<212> DNA

<213> Aquifex aeolicus

<400> 133

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gatacacctt ccttttacgt gtctccaagt aaacaaatat tcaagtgttt cggttgcgagg 180
gtaggggggag acgcgataaa gttcgttttc ctttacgagg acatctccta ttttgaagcc 240
gcccttgaac tcgcaaaacg ctacggaaaag aaattagacc ttgaaaagat atcaaaagac 300
gaaaaggtat acgtggctct tgacaggggt tgtgatttct acagggaag ccttctcaaa 360
aacagagagg caagtgagta cgtaaagagt aggggaatag accctaaagt agcgagggaag 420
tttgatcttg ggtacgcacc ttccagtga gactcgtaa aagtcttaaa agagaacgat 480
cttttagagg cttaccttga aactaaaaac ctcttttctc ctacgaaggg tgtttacagg 540
gatctctttc ttcggcgtgt cgtgatcccg ataaaggatc cgaggggaag agttataggt 600
ttcgggtgaa ggaggatagt agaggacaaa tctccaagt acataaactc tccagacagc 660
agggtattta aaaaggggga gaacttattc ggtctttacg aggcaaagga gtatataaag 720
gaagaaggat ttgcgatact tgtggaaggg tactttgacc ttttgagact tttttccgag 780
ggaataagga acgttgttgc acccctcggg acagccctga cccaaaatca ggcaaacctc 840
ctttccaagt tcacaaaaaa ggtctacatc ctttacgacg gagatgatgc gggaagaaag 900
gctatgaaaa gtgccattcc cctactcctc agtgcaggag tggaagtta tcccgtttac 960
ctccccgaag gatacgaatc cgacgagttt ataaaggaat tcgggaaaga ggaattaaga 1020

```

agactgataa acagctcagg ggagctcttt gaaacgctca taaaaaccgc aagggaac 1080
ttagaggaga aaacgcgtga gttcaggtat tatctgggct ttatttccga tggagtaagg 1140
cgctttgctc tggcttcgga gtttcacacc aagtacaaag ttcctatgga aattttatta 1200
atgaaaattg aaaaaaattc tcaagaaaaa gaaattaaac ttcctttaa ggaaaaaatc 1260
ttcctgaaag gactgataga attaaaacca aaaatagacc ttgaagtcct gaacttaagt 1320
cctgagttaa aggaactcgc agttaacgcc ttaaaccggag aggagcattt acttccaaaa 1380
gaagtctctg agtaccaggt ggataacttg gagaaacttt ttaacaacat ccttagggat 1440
ttacaaaaat ctgggaaaaa gaggaagaaa agagggttga aaaatgtaaa tacttaatta 1500
actttaataa attttttagag ttagga 1526

```

<210> 134

<211> 498

<212> PRT

<213> Aquifex aeolicus

<400> 134

```

Met Ser Ser Asp Ile Asp Glu Leu Arg Arg Glu Ile Asp Ile Val Asp
 1             5             10             15

```

```

Val Ile Ser Glu Tyr Leu Asn Leu Glu Lys Val Gly Ser Asn Tyr Arg
          20             25             30

```

```

Thr Asn Cys Pro Phe His Pro Asp Asp Thr Pro Ser Phe Tyr Val Ser
      35             40             45

```

```

Pro Ser Lys Gln Ile Phe Lys Cys Phe Gly Cys Gly Val Gly Gly Asp
      50             55             60

```

```

Ala Ile Lys Phe Val Ser Leu Tyr Glu Asp Ile Ser Tyr Phe Glu Ala
 65             70             75             80

```

```

Ala Leu Glu Leu Ala Lys Arg Tyr Gly Lys Lys Leu Asp Leu Glu Lys
      85             90             95

```

```

Ile Ser Lys Asp Glu Lys Val Tyr Val Ala Leu Asp Arg Val Cys Asp
     100             105             110

```

```

Phe Tyr Arg Glu Ser Leu Leu Lys Asn Arg Glu Ala Ser Glu Tyr Val
     115             120             125

```

```

Lys Ser Arg Gly Ile Asp Pro Lys Val Ala Arg Lys Phe Asp Leu Gly
     130             135             140

```

```

Tyr Ala Pro Ser Ser Glu Ala Leu Val Lys Val Leu Lys Glu Asn Asp
     145             150             155             160

```

```

Leu Leu Glu Ala Tyr Leu Glu Thr Lys Asn Leu Leu Ser Pro Thr Lys

```

	165		170		175
Gly Val Tyr Arg Asp Leu Phe Leu Arg Arg Val Val Ile Pro Ile Lys					
	180		185		190
Asp Pro Arg Gly Arg Val Ile Gly Phe Gly Gly Arg Arg Ile Val Glu					
	195		200		205
Asp Lys Ser Pro Lys Tyr Ile Asn Ser Pro Asp Ser Arg Val Phe Lys					
	210		215		220
Lys Gly Glu Asn Leu Phe Gly Leu Tyr Glu Ala Lys Glu Tyr Ile Lys					
	225		230		235
Glu Glu Gly Phe Ala Ile Leu Val Glu Gly Tyr Phe Asp Leu Leu Arg					
	245		250		255
Leu Phe Ser Glu Gly Ile Arg Asn Val Val Ala Pro Leu Gly Thr Ala					
	260		265		270
Leu Thr Gln Asn Gln Ala Asn Leu Leu Ser Lys Phe Thr Lys Lys Val					
	275		280		285
Tyr Ile Leu Tyr Asp Gly Asp Asp Ala Gly Arg Lys Ala Met Lys Ser					
	290		295		300
Ala Ile Pro Leu Leu Leu Ser Ala Gly Val Glu Val Tyr Pro Val Tyr					
	305		310		315
Leu Pro Glu Gly Tyr Asp Pro Asp Glu Phe Ile Lys Glu Phe Gly Lys					
	325		330		335
Glu Glu Leu Arg Arg Leu Ile Asn Ser Ser Gly Glu Leu Phe Glu Thr					
	340		345		350
Leu Ile Lys Thr Ala Arg Glu Asn Leu Glu Glu Lys Thr Arg Glu Phe					
	355		360		365
Arg Tyr Tyr Leu Gly Phe Ile Ser Asp Gly Val Arg Arg Phe Ala Leu					
	370		375		380
Ala Ser Glu Phe His Thr Lys Tyr Lys Val Pro Met Glu Ile Leu Leu					
	385		390		395
Met Lys Ile Glu Lys Asn Ser Gln Glu Lys Glu Ile Lys Leu Ser Phe					
	405		410		415
Lys Glu Lys Ile Phe Leu Lys Gly Leu Ile Glu Leu Lys Pro Lys Ile					

420	425	430
Asp Leu Glu Val Leu Asn Leu Ser Pro Glu Leu Lys Glu Leu Ala Val		
435	440	445
Asn Ala Leu Asn Gly Glu Glu His Leu Leu Pro Lys Glu Val Leu Glu		
450	455	460
Tyr Gln Val Asp Asn Leu Glu Lys Leu Phe Asn Asn Ile Leu Arg Asp		
465	470	475
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Leu Gln Lys Ser Gly Lys Lys Arg Lys Lys Arg Gly Leu Lys Asn Val		
485	490	495

Asn Thr

<210> 135
 <211> 705
 <212> DNA
 <213> Aquifex aeolicus

<400> 135

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atcccaaaga	ggtactggaa	cgccaactta	gacacttacc	acccaagaa	cgtatcccag	180
aacagggcac	ttttgacgat	aagggctctc	gtccacaact	tcaatcccga	ggaagggaaa	240
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aaagcgattt	atgagaagaa	gggaatcaga	ggatacttct	tcgatacgaa	ggatctaata	360
ttcagggtta	aacacttaat	ggacgaggga	aaggatacaa	agtttttaaa	aactgtctta	420
aactcacogg	ttttggttct	cgacgacctc	ggttctgaga	ggctcagtga	ctggcagagg	480
gaactcatct	cttacataat	cacttacagg	tataacaacc	ttaagagcac	gataataacc	540
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<210> 136
 <211> 235
 <212> PRT
 <213> Aquifex aeolicus

<400> 136

Met	Gln	Asp	Thr	Ala	Thr	Cys	Ser	Ile	Cys	Gln	Gly	Thr	Gly	Phe	Val
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Lys Thr Glu Asp Asn Lys Val Arg Leu Cys Glu Cys Arg Phe Lys Lys

20	25	30
Arg Asp Val Asn Arg Glu Leu Asn Ile Pro Lys Arg Tyr Trp Asn Ala		
35	40	45
Asn Leu Asp Thr Tyr His Pro Lys Asn Val Ser Gln Asn Arg Ala Leu		
50	55	60
Leu Thr Ile Arg Val Phe Val His Asn Phe Asn Pro Glu Glu Gly Lys		
65	70	75
Gly Leu Thr Phe Val Gly Ser Pro Gly Val Gly Lys Thr His Leu Ala		
85	90	95
Val Ala Thr Leu Lys Ala Ile Tyr Glu Lys Lys Gly Ile Arg Gly Tyr		
100	105	110
Phe Phe Asp Thr Lys Asp Leu Ile Phe Arg Leu Lys His Leu Met Asp		
115	120	125
Glu Gly Lys Asp Thr Lys Phe Leu Lys Thr Val Leu Asn Ser Pro Val		
130	135	140
Leu Val Leu Asp Asp Leu Gly Ser Glu Arg Leu Ser Asp Trp Gln Arg		
145	150	155
Glu Leu Ile Ser Tyr Ile Ile Thr Tyr Arg Tyr Asn Asn Leu Lys Ser		
165	170	175
Thr Ile Ile Thr Thr Asn Tyr Ser Leu Gln Arg Glu Glu Glu Ser Ser		
180	185	190
Val Arg Ile Ser Ala Asp Leu Ala Ser Arg Leu Gly Glu Asn Val Val		
195	200	205
Ser Lys Ile Tyr Glu Met Asn Glu Leu Leu Val Ile Lys Gly Ser Asp		
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Leu Arg Lys Ser Lys Lys Leu Ser Thr Pro Ser		
225	230	235

<210> 137

<211> 4101

<212> DNA

<213> *Thermatoga maritima*

<400> 137

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gatgttgttt	tcaagggaaa	caggctgatt	ctgaaagtgc	ttggagattt	cgcgcgggac	300
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caaccagaaa	agagagaaga	accaaagggg	gaagaattga	agatcgagga	tgaaaaccac	480
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aaaaagacat	cggtgaaggg	caagatcttc	aaaatagaga	agatcgaggg	gaaaagaacg	600
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acggaacagt tcacgctttt c 4101

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<210> 138

<211> 1367

<212> PRT

<213> *Thermatoga maritima*

<400> 138

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Met Lys Lys Ile Glu Asn Leu Lys Trp Lys Asn Val Ser Phe Lys Ser
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Leu Glu Ile Asp Pro Asp Ala Gly Val Val Leu Val Ser Val Glu Lys
      20                      25                      30

```

```

Phe Ser Glu Glu Ile Glu Asp Leu Val Arg Leu Leu Glu Lys Lys Thr
      35                      40                      45

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Arg Phe Arg Val Ile Val Asn Gly Val Gln Lys Ser Asn Gly Asp Leu
      50                      55                      60

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```

Arg Gly Lys Ile Leu Ser Leu Leu Asn Gly Asn Val Pro Tyr Ile Lys
      65                      70                      75                      80

```

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Asp Val Val Phe Glu Gly Asn Arg Leu Ile Leu Lys Val Leu Gly Asp
      85                      90                      95

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Phe Ala Arg Asp Arg Ile Ala Ser Lys Leu Arg Ser Thr Lys Lys Gln

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100	105	110
Leu Asp Glu Leu Leu Pro Pro Gly Thr Glu Ile Met Leu Glu Val Val		
115	120	125
Glu Pro Pro Glu Asp Leu Leu Lys Lys Glu Val Pro Gln Pro Glu Lys		
130	135	140
Arg Glu Glu Pro Lys Gly Glu Glu Leu Lys Ile Glu Asp Glu Asn His		
145	150	155
Ile Phe Gly Gln Lys Pro Arg Lys Ile Val Phe Thr Pro Ser Lys Ile		
	165	170
		175
Phe Glu Tyr Asn Lys Lys Thr Ser Val Lys Gly Lys Ile Phe Lys Ile		
	180	185
		190
Glu Lys Ile Glu Gly Lys Arg Thr Val Leu Leu Ile Tyr Leu Thr Asp		
195	200	205
Gly Glu Asp Ser Leu Ile Cys Lys Val Phe Asn Asp Val Glu Lys Val		
210	215	220
Glu Gly Lys Val Ser Val Gly Asp Val Ile Val Ala Thr Gly Asp Leu		
225	230	235
		240
Leu Leu Glu Asn Gly Glu Pro Thr Leu Tyr Val Lys Gly Ile Thr Lys		
	245	250
		255
Leu Pro Glu Ala Lys Arg Met Asp Lys Ser Pro Val Lys Arg Val Glu		
	260	265
		270
Leu His Ala His Thr Lys Phe Ser Asp Gln Asp Ala Ile Thr Asp Val		
	275	280
		285
Asn Glu Tyr Val Lys Arg Ala Lys Glu Trp Gly Phe Pro Ala Ile Ala		
290	295	300
Leu Thr Asp His Gly Asn Val Gln Ala Ile Pro Tyr Phe Tyr Asp Ala		
305	310	315
		320
Ala Lys Glu Ala Gly Ile Lys Pro Ile Phe Gly Ile Glu Ala Tyr Leu		
	325	330
		335
Val Ser Asp Val Glu Pro Val Ile Arg Asn Leu Ser Asp Asp Ser Thr		
	340	345
		350
Phe Gly Asp Ala Thr Phe Val Val Leu Asp Phe Glu Thr Thr Gly Leu		

355	360	365																	
Asp	Pro	Gln	Val	Asp	Glu	Ile	Ile	Glu	Ile	Gly	Ala	Val	Lys	Ile	Gln				
370						375					380								
Gly	Gly	Gln	Ile	Val	Asp	Glu	Tyr	His	Thr	Leu	Ile	Lys	Pro	Ser	Arg				
385					390					395					400				
Glu	Ile	Ser	Arg	Lys	Ser	Ser	Glu	Ile	Thr	Gly	Ile	Thr	Gln	Glu	Met				
				405					410					415					
Leu	Glu	Asn	Lys	Arg	Ser	Ile	Glu	Glu	Val	Leu	Pro	Glu	Phe	Leu	Gly				
			420					425					430						
Phe	Leu	Glu	Asp	Ser	Ile	Ile	Val	Ala	His	Asn	Ala	Asn	Phe	Asp	Tyr				
	435						440					445							
Arg	Phe	Leu	Arg	Leu	Trp	Ile	Lys	Lys	Val	Met	Gly	Leu	Asp	Trp	Glu				
450						455					460								
Arg	Pro	Tyr	Ile	Asp	Thr	Leu	Ala	Leu	Ala	Lys	Ser	Leu	Leu	Lys	Leu				
465					470					475					480				
Arg	Ser	Tyr	Ser	Leu	Asp	Ser	Val	Val	Glu	Lys	Leu	Gly	Leu	Gly	Pro				
				485					490					495					
Phe	Arg	His	His	Arg	Ala	Leu	Asp	Asp	Ala	Arg	Val	Thr	Ala	Gln	Val				
			500					505					510						
Phe	Leu	Arg	Phe	Val	Glu	Met	Met	Lys	Lys	Ile	Gly	Ile	Thr	Lys	Leu				
	515						520				525								
Ser	Glu	Met	Glu	Lys	Leu	Lys	Asp	Thr	Ile	Asp	Tyr	Thr	Ala	Leu	Lys				
530						535					540								
Pro	Phe	His	Cys	Thr	Ile	Leu	Val	Gln	Asn	Lys	Lys	Gly	Leu	Lys	Asn				
545					550					555					560				
Leu	Tyr	Lys	Leu	Val	Ser	Asp	Ser	Tyr	Ile	Lys	Tyr	Phe	Tyr	Gly	Val				
				565					570					575					
Pro	Arg	Ile	Leu	Lys	Ser	Glu	Leu	Ile	Glu	Asn	Arg	Glu	Gly	Leu	Leu				
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Val	Gly	Ser	Ala	Cys	Ile	Ser	Gly	Glu	Leu	Gly	Arg	Ala	Ala	Leu	Glu				
	595						600					605							
Gly	Ala	Ser	Asp	Ser	Glu	Leu	Glu	Glu	Ile	Ala	Lys	Phe	Tyr	Asp	Tyr				

610				615				620							
Ile	Glu	Val	Met	Pro	Leu	Asp	Val	Ile	Ala	Glu	Asp	Glu	Glu	Asp	Leu
625					630					635				640	
Asp	Arg	Glu	Arg	Leu	Lys	Glu	Val	Tyr	Arg	Lys	Leu	Tyr	Arg	Ile	Ala
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Lys	Lys	Leu	Asn	Lys	Phe	Val	Val	Met	Thr	Gly	Asp	Val	His	Phe	Leu
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		675					680						685		
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	690					695					700				
Glu	Met	Leu	Glu	Lys	Ala	Ile	Glu	Ile	Phe	Glu	Asp	Glu	Glu	Ile	Ala
705					710					715				720	
Arg	Glu	Val	Val	Ile	Glu	Asn	Pro	Asn	Arg	Ile	Ala	Asp	Met	Ile	Glu
				725					730					735	
Glu	Val	Gln	Pro	Leu	Glu	Lys	Lys	Leu	His	Pro	Pro	Ile	Ile	Glu	Asn
			740					745					750		
Ala	Asp	Glu	Ile	Val	Arg	Asn	Leu	Thr	Met	Lys	Arg	Ala	Tyr	Glu	Ile
		755					760						765		
Tyr	Gly	Asp	Pro	Leu	Pro	Glu	Ile	Val	Gln	Lys	Arg	Val	Glu	Lys	Glu
	770					775					780				
Leu	Asn	Ala	Ile	Ile	Asn	His	Gly	Tyr	Ala	Val	Leu	Tyr	Leu	Ile	Ala
785					790					795				800	
Gln	Glu	Leu	Val	Gln	Lys	Ser	Met	Ser	Asp	Gly	Tyr	Val	Val	Gly	Ser
			805						810					815	
Arg	Gly	Ser	Val	Gly	Ser	Ser	Leu	Val	Ala	Asn	Leu	Leu	Gly	Ile	Thr
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Glu	Val	Asn	Pro	Leu	Pro	Pro	His	Tyr	Arg	Cys	Pro	Glu	Cys	Lys	Tyr
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Phe	Glu	Val	Val	Glu	Asp	Asp	Arg	Tyr	Gly	Ala	Gly	Tyr	Asp	Leu	Pro
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Asn	Lys	Asn	Cys	Pro	Arg	Cys	Gly	Ala	Pro	Leu	Arg	Lys	Asp	Gly	His

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Gly Ile Pro Phe Glu Thr Phe Met Gly Phe Glu Gly Asp Lys Val Pro						
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Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Glu Arg Ala His Arg						
	900			905		910
Phe Val Glu Glu Leu Phe Gly Lys Asp His Val Tyr Arg Ala Gly Thr						
	915			920		925
Ile Asn Thr Ile Ala Glu Arg Ser Ala Val Gly Tyr Val Arg Ser Tyr						
	930			935		940
Glu Glu Lys Thr Gly Lys Lys Leu Arg Lys Ala Glu Met Glu Arg Leu						
945		950		955		960
Val Ser Met Ile Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro Gly						
	965			970		975
Gly Leu Met Ile Ile Pro Lys Asp Lys Glu Val Tyr Asp Phe Thr Pro						
	980			985		990
Ile Gln Tyr Pro Ala Asn Asp Arg Asn Ala Gly Val Phe Thr Thr His						
	995			1000		1005
Phe Ala Tyr Glu Thr Ile His Asp Asp Leu Val Lys Ile Asp Ala Leu						
1010		1015		1020		
Gly His Asp Asp Pro Thr Phe Ile Lys Met Leu Lys Asp Leu Thr Gly						
1025		1030		1035		1040
Ile Asp Pro Met Thr Ile Pro Met Asp Asp Pro Asp Thr Leu Ala Ile						
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Phe Ser Ser Val Lys Pro Leu Gly Val Asp Pro Val Glu Leu Glu Ser						
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Asp Val Gly Thr Tyr Gly Ile Pro Glu Phe Gly Thr Glu Phe Val Arg						
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Gly Met Leu Val Glu Thr Arg Pro Lys Ser Phe Ala Glu Leu Val Arg						
1090		1095		1100		
Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Asn Asn Ala Arg						
1105		1110		1115		1120
Asp Trp Ile Asn Leu Gly Tyr Ala Lys Leu Ser Glu Val Ile Ser Cys						

1125	1130	1135
Arg Asp Asp Ile Met Asn Phe Leu Ile His Lys Gly Met Glu Pro Ser		
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Leu Ala Phe Lys Ile Met Glu Asn Val Arg Lys Gly Lys Gly Ile Thr		
1155	1160	1165
Glu Glu Met Glu Ser Glu Met Arg Arg Leu Lys Val Pro Glu Trp Phe		
1170	1175	1180
Ile Glu Ser Cys Lys Arg Ile Lys Tyr Leu Phe Pro Lys Ala His Ala		
1185	1190	1195 1200
Val Ala Tyr Val Ser Met Ala Phe Arg Ile Ala Tyr Phe Lys Val His		
1205	1210	1215
Tyr Pro Leu Gln Phe Tyr Ala Ala Tyr Phe Thr Ile Lys Gly Asp Gln		
1220	1225	1230
Phe Asp Pro Val Leu Val Leu Arg Gly Lys Glu Ala Ile Lys Arg Arg		
1235	1240	1245
Leu Arg Glu Leu Lys Ala Met Pro Ala Lys Asp Ala Gln Lys Lys Asn		
1250	1255	1260
Glu Val Ser Val Leu Glu Val Ala Leu Glu Met Ile Leu Arg Gly Phe		
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Ser Phe Leu Pro Pro Asp Ile Phe Lys Ser Asp Ala Lys Lys Phe Leu		
1285	1290	1295
Ile Glu Gly Asn Ser Leu Arg Ile Pro Phe Asn Lys Leu Pro Gly Leu		
1300	1305	1310
Gly Asp Ser Val Ala Glu Ser Ile Ile Arg Ala Arg Glu Glu Lys Pro		
1315	1320	1325
Phe Thr Ser Val Glu Asp Leu Met Lys Arg Thr Lys Val Asn Lys Asn		
1330	1335	1340
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1365		

<210> 139
 <211> 567
 <212> DNA
 <213> *Thermatoga maritima*

<400> 139
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 aacttcgacc tcacttttct ggatatgatg gcaaaggaaa cgggaaactt tccaataacg 360
 aatccctaca tcgacacact cgatctttca gaagagatct ttggaaggcc tcattctctc 420
 aaatggctct ccgaaagact tggaataaaa accacgatac ggcaccgtgc tcttccagat 480
 gccctggtga ccgcaagagt ttttgtgaag cttgttgaat ttcttggtga aaacaggggc 540
 aacgaattca tacgtggaaa acggggg 567

<210> 140
 <211> 189
 <212> PRT
 <213> *Thermatoga maritima*

<400> 140
 Met Leu Ala Met Ile Trp Asn Asp Thr Val Phe Cys Val Val Asp Thr
 1 5 10 15
 Glu Thr Thr Gly Thr Asp Pro Phe Ala Gly Asp Arg Ile Val Glu Ile
 20 25 30
 Ala Ala Val Pro Val Phe Lys Gly Lys Ile Tyr Arg Asn Lys Ala Phe
 35 40 45
 His Ser Leu Val Asn Pro Arg Ile Arg Ile Pro Ala Leu Ile Gln Lys
 50 55 60
 Val His Gly Ile Ser Asn Met Asp Ile Val Glu Ala Pro Asp Met Asp
 65 70 75 80
 Thr Val Tyr Asp Leu Phe Arg Asp Tyr Val Lys Gly Thr Val Leu Val
 85 90 95
 Phe His Asn Ala Asn Phe Asp Leu Thr Phe Leu Asp Met Met Ala Lys
 100 105 110
 Glu Thr Gly Asn Phe Pro Ile Thr Asn Pro Tyr Ile Asp Thr Leu Asp
 115 120 125

Leu Ser Glu Glu Ile Phe Gly Arg Pro His Ser Leu Lys Trp Leu Ser
 130 135 140

Glu Arg Leu Gly Ile Lys Thr Thr Ile Arg His Arg Ala Leu Pro Asp
 145 150 155 160

Ala Leu Val Thr Ala Arg Val Phe Val Lys Leu Val Glu Phe Leu Gly
 165 170 175

Glu Asn Arg Val Asn Glu Phe Ile Arg Gly Lys Arg Gly
 180 185

<210> 141

<211> 1434

<212> DNA

<213> *Thermatoga maritima*

<400> 141

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catgtgaaga aggcaataat cgggtgctatt cagaagaaca gcgtggccca cggatacata 120
ttcgccggtc cgaggggaac ggggaagact actcttgcca gaattctcgc aaaatccctg 180
aactgtgaga acagaaaggg agttgaaccc tgcaattcct gcagagcctg cagagagata 240
gacgagggaa ccttcatgga cgtgatagag ctcgacgcgg cctccaacag aggaatagac 300
gagatcagaa gaatcagaga cgccgttgga tacaggccga tggaaggtaa atacaaagtc 360
tacataatag acgaagttca catgctcacg aaagaagcct tcaacgcgct cctcaaaaca 420
ctcgaagaac ctccctccca cgtcgtgttc gtgctggcaa cgacaaacct tgagaaggtt 480
cctcccacga ttatctcgag atgtcaggtt ttcgagttca gaaacattcc cgacgagctc 540
atcgaaaaga ggctccagga agttgctggag gctgaaggaa tagagataga cagggaagct 600
ctgagcttca tcgcaaaaag agcctctgga ggcttgagag acgcgctcac catgctcgag 660
caggtgtgga agttctcgga aggaaagata gatctcgaga cggtagacag ggcgctcggg 720
ttgataccga tacaggttgt tcgcgattac gtgaacgcta tcttttctgg tgatgtgaaa 780
agggtcttca ccgttctcga cgacgtctat tacagcgga aggactacga ggtgctcatt 840
caggaagcag tcgaggatct ggtcgaagac ctggaaaggg agagaggggt ttaccaggtt 900
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cagaaagaag agaagaaaga aacggtgaag gcaaaagaag aaaaacagga agacagcgag 1140
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gattcatcga aagctatgca ttacgagttg atgaagaaaa aactgcctga gctggaaaac 1320
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gaaacaatcg agaaggtttc tcagaagatc ctgagattgt ttgaacagga ggga 1434
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<210> 142

<211> 478

<212> PRT

<213> *Thermatoga maritima*

<400> 142

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  1              5              10              15

Val Asn Gln Asp His Val Lys Lys Ala Ile Ile Gly Ala Ile Gln Lys
      20              25              30

Asn Ser Val Ala His Gly Tyr Ile Phe Ala Gly Pro Arg Gly Thr Gly
      35              40              45

Lys Thr Thr Leu Ala Arg Ile Leu Ala Lys Ser Leu Asn Cys Glu Asn
      50              55              60

Arg Lys Gly Val Glu Pro Cys Asn Ser Cys Arg Ala Cys Arg Glu Ile
      65              70              75              80

Asp Glu Gly Thr Phe Met Asp Val Ile Glu Leu Asp Ala Ala Ser Asn
      85              90              95

Arg Gly Ile Asp Glu Ile Arg Arg Ile Arg Asp Ala Val Gly Tyr Arg
      100             105             110

Pro Met Glu Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Val His Met
      115             120             125

Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro
      130             135             140

Pro Ser His Val Val Phe Val Leu Ala Thr Thr Asn Leu Glu Lys Val
      145             150             155             160

Pro Pro Thr Ile Ile Ser Arg Cys Gln Val Phe Glu Phe Arg Asn Ile
      165             170             175

Pro Asp Glu Leu Ile Glu Lys Arg Leu Gln Glu Val Ala Glu Ala Glu
      180             185             190

Gly Ile Glu Ile Asp Arg Glu Ala Leu Ser Phe Ile Ala Lys Arg Ala
      195             200             205

Ser Gly Gly Leu Arg Asp Ala Leu Thr Met Leu Glu Gln Val Trp Lys
      210             215             220

Phe Ser Glu Gly Lys Ile Asp Leu Glu Thr Val His Arg Ala Leu Gly
      225             230             235             240
```

Leu Ile Pro Ile Gln Val Val Arg Asp Tyr Val Asn Ala Ile Phe Ser
245 250 255

Gly Asp Val Lys Arg Val Phe Thr Val Leu Asp Asp Val Tyr Tyr Ser
260 265 270

Gly Lys Asp Tyr Glu Val Leu Ile Gln Glu Ala Val Glu Asp Leu Val
275 280 285

Glu Asp Leu Glu Arg Glu Arg Gly Val Tyr Gln Val Ser Ala Asn Asp
290 295 300

Ile Val Gln Val Ser Arg Gln Leu Leu Asn Leu Leu Arg Glu Ile Lys
305 310 315 320

Phe Ala Glu Glu Lys Arg Leu Val Cys Lys Val Gly Ser Ala Tyr Ile
325 330 335

Ala Thr Arg Phe Ser Thr Thr Asn Val Gln Glu Asn Asp Val Arg Glu
340 345 350

Lys Asn Asp Asn Ser Asn Val Gln Gln Lys Glu Glu Lys Lys Glu Thr
355 360 365

Val Lys Ala Lys Glu Glu Lys Gln Glu Asp Ser Glu Phe Glu Lys Arg
370 375 380

Phe Lys Glu Leu Met Glu Glu Leu Lys Glu Lys Gly Asp Leu Ser Ile
385 390 395 400

Phe Val Ala Leu Ser Leu Ser Glu Val Gln Phe Asp Gly Glu Lys Val
405 410 415

Ile Ile Ser Phe Asp Ser Ser Lys Ala Met His Tyr Glu Leu Met Lys
420 425 430

Lys Lys Leu Pro Glu Leu Glu Asn Ile Phe Ser Arg Lys Leu Gly Lys
435 440 445

Lys Val Glu Val Glu Leu Arg Leu Met Gly Lys Glu Glu Thr Ile Glu
450 455 460

Lys Val Ser Gln Lys Ile Leu Arg Leu Phe Glu Gln Glu Gly
465 470 475

<210> 143

<211> 1098

<212> DNA

<213> *Thermatoga maritima*

<400> 143

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ctcgcaaaga aatccgtgaa acccattctt gctggatttc ttttcgaagt gaaagatgga 120
aattttctaca tctgcgcgac cgatctcgag accggagtca aagcaaccgt gaatgccgct 180
gaaatctccg gtgaggcacg ttttgtggta ccaggagatg tcattcagaa gatgggtcaag 240
gttctcccag atgagataac ggaactttct ttagaggggg atgctcttgt tataagttct 300
ggaagcaccg ttttcaggat caccaccatg cccgcggacg aatttccaga gataacgcct 360
gccgagtctg gaataacctt cgaagttgac acttcgctcc tcgaggaaat ggttgaaaag 420
gtcatcttcg ccgctgccaa agacgagttc atgcgaaatc tgaatggagt tttctgggaa 480
ctccacaaga atcttctcag gctggttgca agtgatggtt tcagacttgc acttgctgaa 540
gagcagatag aaaacgagga agaggcgagt ttcttgctct ctttgaagag catgaaagaa 600
gttcaaaaacg tgctggacaa cacaacggag ccgactataa cggtgaggta cgatggaaga 660
aggggtttctc tgctgacaaa tgatgtagaa acgggtgatg gagtggtcga cgctgaatth 720
cccgattaca aaagggtgat ccccgaaact ttcaaaacga aagtgggtgt ttccagaaaa 780
gaactcaggg aatctttgaa gaggggtgat gtgattgcca gcaagggaag cgagtccgtg 840
aagttcgaaa tagaagaaaa cgttatgaga cttgtgagca agagcccgga ttatggagaa 900
gtggtcgatg aagttgaagt tcaaaaagaa ggggaagatc tcgtgatcgc tttcaacccg 960
aagttcatcg aggacgtttt gaagcacatt gagactgaag aaatcgaaat gaacttcgtt 1020
gattctacca gtccatgtca gataaatcca ctcgatattt ctggatacct ttacatagtg 1080
atgcccacatca gactggca 1098
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<210> 144

<211> 366

<212> PRT

<213> *Thermatoga maritima*

<400> 144

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Met Lys Val Thr Val Thr Thr Leu Glu Leu Lys Asp Lys Ile Thr Ile
  1              5              10              15


Ala Ser Lys Ala Leu Ala Lys Lys Ser Val Lys Pro Ile Leu Ala Gly
      20              25              30

Phe Leu Phe Glu Val Lys Asp Gly Asn Phe Tyr Ile Cys Ala Thr Asp
      35              40              45

Leu Glu Thr Gly Val Lys Ala Thr Val Asn Ala Ala Glu Ile Ser Gly
      50              55              60

Glu Ala Arg Phe Val Val Pro Gly Asp Val Ile Gln Lys Met Val Lys
      65              70              75              80

Val Leu Pro Asp Glu Ile Thr Glu Leu Ser Leu Glu Gly Asp Ala Leu
      85              90              95
```



Val	Ile	Ser	Ser	Gly	Ser	Thr	Val	Phe	Arg	Ile	Thr	Thr	Met	Pro	Ala			
			100					105					110					
Asp	Glu	Phe	Pro	Glu	Ile	Thr	Pro	Ala	Glu	Ser	Gly	Ile	Thr	Phe	Glu			
		115					120					125						
Val	Asp	Thr	Ser	Leu	Leu	Glu	Glu	Met	Val	Glu	Lys	Val	Ile	Phe	Ala			
	130					135					140							
Ala	Ala	Lys	Asp	Glu	Phe	Met	Arg	Asn	Leu	Asn	Gly	Val	Phe	Trp	Glu			
145					150				155						160			
Leu	His	Lys	Asn	Leu	Leu	Arg	Leu	Val	Ala	Ser	Asp	Gly	Phe	Arg	Leu			
			165					170						175				
Ala	Leu	Ala	Glu	Glu	Gln	Ile	Glu	Asn	Glu	Glu	Glu	Ala	Ser	Phe	Leu			
			180					185					190					
Leu	Ser	Leu	Lys	Ser	Met	Lys	Glu	Val	Gln	Asn	Val	Leu	Asp	Asn	Thr			
	195						200					205						
Thr	Glu	Pro	Thr	Ile	Thr	Val	Arg	Tyr	Asp	Gly	Arg	Arg	Val	Ser	Leu			
	210					215					220							
Ser	Thr	Asn	Asp	Val	Glu	Thr	Val	Met	Arg	Val	Val	Asp	Ala	Glu	Phe			
225					230					235					240			
Pro	Asp	Tyr	Lys	Arg	Val	Ile	Pro	Glu	Thr	Phe	Lys	Thr	Lys	Val	Val			
			245						250					255				
Val	Ser	Arg	Lys	Glu	Leu	Arg	Glu	Ser	Leu	Lys	Arg	Val	Met	Val	Ile			
		260					265						270					
Ala	Ser	Lys	Gly	Ser	Glu	Ser	Val	Lys	Phe	Glu	Ile	Glu	Glu	Asn	Val			
		275					280					285						
Met	Arg	Leu	Val	Ser	Lys	Ser	Pro	Asp	Tyr	Gly	Glu	Val	Val	Asp	Glu			
	290					295					300							
Val	Glu	Val	Gln	Lys	Glu	Gly	Glu	Asp	Leu	Val	Ile	Ala	Phe	Asn	Pro			
305					310					315					320			
Lys	Phe	Ile	Glu	Asp	Val	Leu	Lys	His	Ile	Glu	Thr	Glu	Glu	Ile	Glu			
			325					330						335				
Met	Asn	Phe	Val	Asp	Ser	Thr	Ser	Pro	Cys	Gln	Ile	Asn	Pro	Leu	Asp			
		340						345					350					

Ile Ser Gly Tyr Leu Tyr Ile Val Met Pro Ile Arg Leu Ala
 355 360 365

<210> 145
 <211> 972
 <212> DNA
 <213> *Thermatoga maritima*

<400> 145
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 ctctgaagg atggtaacgt ggagtacata aggatccatc cggaggatcc cgacaagatc 120
 gatttcataa ggtctttact caggacaaag acgatctttt ccaacaagac gatcattgac 180
 atcgtcaatt tcgatgagt gaaagcacag gagcagaagc gtctcgttga acttttgaaa 240
 aacgtaccgg aagacgttca tatcttcac cgttctcaaa aaacagggtgg aaagggagta 300
 gcgctggagc ttccgaagcc atgggaaacg gacaagtggc ttgagtggat agaaaagcgc 360
 ttcagggaga atggtttgct catcgataaa gatgccttc agctgttttt ctccaagggt 420
 ggaacgaacg acctgatcat agaaagggag attgaaaaac tgaaagctta ttccgaggac 480
 agaaagataa cggtagaaga cgtggaagag gtcgttttta cctatcagac tccgggatac 540
 gatgattttt gctttgctgt ttccgaagga aaaaggaagc tcgctcactc tcttctgtcg 600
 cagctgtgga aaaccacaga gtccgtggtg attgccactg tccttgcgaa tcacttcttg 660
 gatctcttca aaatcctcgt tcttgtgaca aagaaaagat actacacctg gcctgatgtg 720
 tccagggtgt ccaaagagct gggaattccc gttcctcgtg tggctcgttt cctcggtttc 780
 tcctttaaga cctggaaatt caaggtgatg aaccacctcc tctactacga tgtgaagaag 840
 gtagaaaga tactgaggga tctctacgat ctggacagag ccgtgaaaag cgaagaagat 900
 ccaaaaccgt tcttccacga gttcatagaa gaggtggcac tggatgtata ttctcttcag 960
 agagatgaag aa 972

<210> 146
 <211> 324
 <212> PRT
 <213> *Thermatoga maritima*

<400> 146
 Met Pro Val Thr Phe Leu Thr Gly Thr Ala Glu Thr Gln Lys Glu Glu
 1 5 10 15
 Leu Ile Lys Lys Leu Leu Lys Asp Gly Asn Val Glu Tyr Ile Arg Ile
 20 25 30
 His Pro Glu Asp Pro Asp Lys Ile Asp Phe Ile Arg Ser Leu Leu Arg
 35 40 45
 Thr Lys Thr Ile Phe Ser Asn Lys Thr Ile Ile Asp Ile Val Asn Phe
 50 55 60

Asp Glu Trp Lys Ala Gln Glu Gln Lys Arg Leu Val Glu Leu Leu Lys
 65 70 75 80
 Asn Val Pro Glu Asp Val His Ile Phe Ile Arg Ser Gln Lys Thr Gly
 85 90 95
 Gly Lys Gly Val Ala Leu Glu Leu Pro Lys Pro Trp Glu Thr Asp Lys
 100 105 110
 Trp Leu Glu Trp Ile Glu Lys Arg Phe Arg Glu Asn Gly Leu Leu Ile
 115 120 125
 Asp Lys Asp Ala Leu Gln Leu Phe Phe Ser Lys Val Gly Thr Asn Asp
 130 135 140
 Leu Ile Ile Glu Arg Glu Ile Glu Lys Leu Lys Ala Tyr Ser Glu Asp
 145 150 155 160
 Arg Lys Ile Thr Val Glu Asp Val Glu Glu Val Val Phe Thr Tyr Gln
 165 170 175
 Thr Pro Gly Tyr Asp Asp Phe Cys Phe Ala Val Ser Glu Gly Lys Arg
 180 185 190
 Lys Leu Ala His Ser Leu Leu Ser Gln Leu Trp Lys Thr Thr Glu Ser
 195 200 205
 Val Val Ile Ala Thr Val Leu Ala Asn His Phe Leu Asp Leu Phe Lys
 210 215 220
 Ile Leu Val Leu Val Thr Lys Lys Arg Tyr Tyr Thr Trp Pro Asp Val
 225 230 235 240
 Ser Arg Val Ser Lys Glu Leu Gly Ile Pro Val Pro Arg Val Ala Arg
 245 250 255
 Phe Leu Gly Phe Ser Phe Lys Thr Trp Lys Phe Lys Val Met Asn His
 260 265 270
 Leu Leu Tyr Tyr Asp Val Lys Lys Val Arg Lys Ile Leu Arg Asp Leu
 275 280 285
 Tyr Asp Leu Asp Arg Ala Val Lys Ser Glu Glu Asp Pro Lys Pro Phe
 290 295 300
 Phe His Glu Phe Ile Glu Glu Val Ala Leu Asp Val Tyr Ser Leu Gln
 305 310 315 320

Arg Asp Glu Glu

<210> 147

<211> 936

<212> DNA

<213> *Thermatoga maritima*

<400> 147

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gtatcccttg aacttcccga gtacgtggag aaatttcccc cgaaggcctc ggatgttctg 180
gagatagatc ccgaggggga gaacataggc atagacgaca tcagaacgat aaaggacttc 240
ctgaactaca gccccgagct ctacacgaga aagtacgtga tagtccacga ctgtgaaaga 300
atgacccagc aggcggcgaa cgcgtttctg aaggcccttg aagaaccacc agaatacgct 360
gtgatcgctc tgaacactcg ccgctggcat tatctactgc cgacgataaa gagccgagtg 420
ttcagagtgg ttgtgaacgt tccaaaggag ttcagagatc tcgtgaaaga gaaaatagga 480
gatctctggg aggaacttcc acttcttgag agagacttca aaacggctct cgaagcctac 540
aaacttggtg cggaaaaact ttctggattg atggaaagtc tcaaagtttt ggagacggaa 600
aaactcttga aaaaggtcct ttcaaaaggc ctggaagggt atctcgcatg tagggagctc 660
ctggagagat tttcaaagggt ggaatcgaag gaattctttg cgctttttga tcagggtgact 720
aacacgataa caggaaaaga cgcgtttctt ttgatccaga gactgacaag aatcattctc 780
cacgaaaaca catgggaaag cgttgaagat caaaaaagcg tgtctttcct cgattcaatt 840
ctcagggtga agatagcgaa tctgaacaac aaactcactc tgatgaacat cctcgcgata 900
cacagagaga gaaagagagg tgtcaacgct tggagc 936
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<210> 148

<211> 311

<212> PRT

<213> *Thermatoga maritima*

<400> 148

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Met Asn Asp Leu Ile Arg Lys Tyr Ala Lys Asp Gln Leu Glu Thr Leu
  1             5             10             15

Lys Arg Ile Ile Glu Lys Ser Glu Gly Ile Ser Ile Leu Ile Asn Gly
      20             25             30

Glu Asp Leu Ser Tyr Pro Arg Glu Val Ser Leu Glu Leu Pro Glu Tyr
      35             40             45

Val Glu Lys Phe Pro Pro Lys Ala Ser Asp Val Leu Glu Ile Asp Pro
      50             55             60

Glu Gly Glu Asn Ile Gly Ile Asp Asp Ile Arg Thr Ile Lys Asp Phe
      65             70             75             80
```

Leu	Asn	Tyr	Ser	Pro	Glu	Leu	Tyr	Thr	Arg	Lys	Tyr	Val	Ile	Val	His	85	90	95
Asp	Cys	Glu	Arg	Met	Thr	Gln	Gln	Ala	Ala	Asn	Ala	Phe	Leu	Lys	Ala	100	105	110
Leu	Glu	Glu	Pro	Pro	Glu	Tyr	Ala	Val	Ile	Val	Leu	Asn	Thr	Arg	Arg	115	120	125
Trp	His	Tyr	Leu	Leu	Pro	Thr	Ile	Lys	Ser	Arg	Val	Phe	Arg	Val	Val	130	135	140
Val	Asn	Val	Pro	Lys	Glu	Phe	Arg	Asp	Leu	Val	Lys	Glu	Lys	Ile	Gly	145	150	155
Asp	Leu	Trp	Glu	Glu	Leu	Pro	Leu	Leu	Glu	Arg	Asp	Phe	Lys	Thr	Ala	165	170	175
Leu	Glu	Ala	Tyr	Lys	Leu	Gly	Ala	Glu	Lys	Leu	Ser	Gly	Leu	Met	Glu	180	185	190
Ser	Leu	Lys	Val	Leu	Glu	Thr	Glu	Lys	Leu	Leu	Lys	Lys	Val	Leu	Ser	195	200	205
Lys	Gly	Leu	Glu	Gly	Tyr	Leu	Ala	Cys	Arg	Glu	Leu	Leu	Glu	Arg	Phe	210	215	220
Ser	Lys	Val	Glu	Ser	Lys	Glu	Phe	Phe	Ala	Leu	Phe	Asp	Gln	Val	Thr	225	230	235
Asn	Thr	Ile	Thr	Gly	Lys	Asp	Ala	Phe	Leu	Leu	Ile	Gln	Arg	Leu	Thr	245	250	255
Arg	Ile	Ile	Leu	His	Glu	Asn	Thr	Trp	Glu	Ser	Val	Glu	Asp	Lys	Ser	260	265	270
Val	Ser	Phe	Leu	Asp	Ser	Ile	Leu	Arg	Val	Lys	Ile	Ala	Asn	Leu	Asn	275	280	285
Asn	Lys	Leu	Thr	Leu	Met	Asn	Ile	Leu	Ala	Ile	His	Arg	Glu	Arg	Lys	290	295	300
Arg	Gly	Val	Asn	Ala	Trp	Ser										305	310	

<210> 149

<211> 423
 <212> DNA
 <213> *Thermatoga maritima*

<400> 149
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 aagaacgcgc cggacgacgc tcaaacgact gatttcttca ggatcggtcac ctttggaaga 180
 ctggcagagt tcgctagaac ctatctcacc aaaggaaggc tcgttctcgt cgaaggtgaa 240
 atgagaatga gaagatggga aacaccact ggagaaaaga gggtagctcc ggaggtgtgc 300
 gcaaacggtg ttagattcat ggacagaaaa cctgctgaaa cagttagcga gactgaagag 360
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 ttt 423

<210> 150
 <211> 141
 <212> PRT
 <213> *Thermatoga maritima*

<400> 150
 Met Ser Phe Phe Asn Lys Ile Ile Leu Ile Gly Arg Leu Val Arg Asp
 1 5 10 15
 Pro Glu Glu Arg Tyr Thr Leu Ser Gly Thr Pro Val Thr Thr Phe Thr
 20 25 30
 Ile Ala Val Asp Arg Val Pro Arg Lys Asn Ala Pro Asp Asp Ala Gln
 35 40 45
 Thr Thr Asp Phe Phe Arg Ile Val Thr Phe Gly Arg Leu Ala Glu Phe
 50 55 60
 Ala Arg Thr Tyr Leu Thr Lys Gly Arg Leu Val Leu Val Glu Gly Glu
 65 70 75 80
 Met Arg Met Arg Arg Trp Glu Thr Pro Thr Gly Glu Lys Arg Val Ser
 85 90 95
 Pro Glu Val Val Ala Asn Val Val Arg Phe Met Asp Arg Lys Pro Ala
 100 105 110
 Glu Thr Val Ser Glu Thr Glu Glu Glu Leu Glu Ile Pro Glu Glu Asp
 115 120 125
 Phe Ser Ser Asp Thr Phe Ser Glu Asp Glu Pro Pro Phe
 130 135 140

<210> 151
 <211> 1353
 <212> DNA
 <213> *Thermatoga maritima*

<400> 151
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 aaacaccaac acatcttcag agcgatggaa gagctttacg acgaaggaaa accggtggac 180
 gtggtttccg tctgtgacaa gcttcaaagc atgggaaaac tcgaggaagt aggtggagat 240
 ctggaagtgg cccagctcgc tgaggctgtg cccagttctg cacacgcact tcactacgcg 300
 gagatcgtca aggaaaaatc cattctgagg aaactcattg agatctccag aaaaatctca 360
 gaaagtgcct acatggaaga agatgtggag atcctgctcg acaacgcaga aaagatgata 420
 ttcgagatct cagagatgaa aacgacaaaa tcctacgata atctgagagg catcatgcac 480
 cgggtgtttg aaaacctgga gaacttcagg gaaagagcca acctataga acccgggtgtg 540
 ctcataacgg gactaccaac gggattcaaa agtctggaca aacagaccac agggttccac 600
 agctccgatac tggatgataat agcagcgaga cctccatgg gaaaaacctc ctccgcactc 660
 tcaatagcga ggaacatggc tgtcaatttc gaaatccccg tcggaatatt cagtctcgag 720
 atgtccaagg aacagctcgc tcaaagacta ctcagcatgg agtccggtgt ggatctttac 780
 agcatcagaa caggatacct ggatcaggag aagtgggaaa gactcacaat agcggtttct 840
 aaactctaca aagcaccatc agttgtggac gatgagtcac tcctcgatcc gcgatcgttg 900
 agggcaaaaag cgagaaggat gaaaaaagaa tacgatgtaa aagccatttt tgtcgactat 960
 ctccagctca tgcacctgaa aggaagaaaa gaaagcagac agcaggagat atccgagatc 1020
 tcgagatctc tgaagctcct tgcgagggaa ctcgacatag tggatgtagc gctttcacag 1080
 ctttcgaggg ccgtagaaca gagagaagac aaaagaccga ggctgagtga cctcagggaa 1140
 tccggtgcga tagaacagga cgcagacaca gtcattctca tctacaggga ggaatattac 1200
 aggagcaaaa aatccaaaga ggaaagcaag cttcacgaac ctcacgaagc tgaaatcata 1260
 ataggtaaac agagaaacgg tcccgttgga acgatcactc tgatcttcga cccagaacg 1320
 gttacgttcc atgaagtcga tgtggtgcat tca 1353

<210> 152
 <211> 451
 <212> PRT
 <213> *Thermatoga maritima*

<400> 152
 Met Arg Val Pro Pro His Asn Leu Glu Ala Glu Val Ala Val Leu Gly
 1 5 10 15
 Ser Ile Leu Ile Asp Pro Ser Val Ile Asn Asp Val Leu Glu Ile Leu
 20 25 30
 Ser His Glu Asp Phe Tyr Leu Lys Lys His Gln His Ile Phe Arg Ala
 35 40 45
 Met Glu Glu Leu Tyr Asp Glu Gly Lys Pro Val Asp Val Val Ser Val

50					55					60					
Cys	Asp	Lys	Leu	Gln	Ser	Met	Gly	Lys	Leu	Glu	Glu	Val	Gly	Gly	Asp
65					70					75					80
Leu	Glu	Val	Ala	Gln	Leu	Ala	Glu	Ala	Val	Pro	Ser	Ser	Ala	His	Ala
				85					90					95	
Leu	His	Tyr	Ala	Glu	Ile	Val	Lys	Glu	Lys	Ser	Ile	Leu	Arg	Lys	Leu
			100					105					110		
Ile	Glu	Ile	Ser	Arg	Lys	Ile	Ser	Glu	Ser	Ala	Tyr	Met	Glu	Glu	Asp
		115					120					125			
Val	Glu	Ile	Leu	Leu	Asp	Asn	Ala	Glu	Lys	Met	Ile	Phe	Glu	Ile	Ser
	130					135					140				
Glu	Met	Lys	Thr	Thr	Lys	Ser	Tyr	Asp	His	Leu	Arg	Gly	Ile	Met	His
145					150					155					160
Arg	Val	Phe	Glu	Asn	Leu	Glu	Asn	Phe	Arg	Glu	Arg	Ala	Asn	Leu	Ile
				165					170					175	
Glu	Pro	Gly	Val	Leu	Ile	Thr	Gly	Leu	Pro	Thr	Gly	Phe	Lys	Ser	Leu
			180					185					190		
Asp	Lys	Gln	Thr	Thr	Gly	Phe	His	Ser	Ser	Asp	Leu	Val	Ile	Ile	Ala
		195					200					205			
Ala	Arg	Pro	Ser	Met	Gly	Lys	Thr	Ser	Phe	Ala	Leu	Ser	Ile	Ala	Arg
	210					215					220				
Asn	Met	Ala	Val	Asn	Phe	Glu	Ile	Pro	Val	Gly	Ile	Phe	Ser	Leu	Glu
225					230					235					240
Met	Ser	Lys	Glu	Gln	Leu	Ala	Gln	Arg	Leu	Leu	Ser	Met	Glu	Ser	Gly
				245					250					255	
Val	Asp	Leu	Tyr	Ser	Ile	Arg	Thr	Gly	Tyr	Leu	Asp	Gln	Glu	Lys	Trp
			260					265					270		
Glu	Arg	Leu	Thr	Ile	Ala	Ala	Ser	Lys	Leu	Tyr	Lys	Ala	Pro	Ile	Val
		275					280					285			
Val	Asp	Asp	Glu	Ser	Leu	Leu	Asp	Pro	Arg	Ser	Leu	Arg	Ala	Lys	Ala
	290					295					300				
Arg	Arg	Met	Lys	Lys	Glu	Tyr	Asp	Val	Lys	Ala	Ile	Phe	Val	Asp	Tyr


```

aaaaaagtgg caaaagaggt tggttttttc gtcattcaccg aaggctactt cgacgcgctc 780
gcattcagaa aggatggaat accaacggcg gtcgctgttc ttggggcgag tctttcaaga 840
gaggcgattc taaaactttc ggcgatttcg aaaaacgtca tactgtgttt cgataatgac 900
aaagcaggct tcagagccac tctcaaatcc ctcgaggatc tcctagacta cgaattcaac 960
gtgcttgttg caaccccttc tccttcaaaa gaccagatg aactctttca gaaagaagga 1020
gaaggttcat tgaaaaagat gctgaaaaac tcgcgttcgt tcgaatatTT tctggtgacg 1080
gctggtgagg tcttctttga caggaacagc cccgcgggtg tgagatccta cctttctttc 1140
ctcaaagggt gggtcacaaa gatgagaagg aaaggatatt tgaaacacat agaaaatctc 1200
gtgaatgagg tttcatcttc tctccagata ccagaaaacc agattttgaa cttttttgaa 1260
agcgacagggt ctaacactat gcctgttcat gagaccaagt cgtcaaagggt ttacgatgag 1320
gggagaggac tggcttattt gtttttgaac tacgaggatt tgaggggaaaa gattctggaa 1380
ctggacttag aggtactgga agataaaaaac gcgagggagt tttcaagag agtctcactg 1440
ggagaagatt tgaacaaagt catagaaaac ttcccaaaag agctgaaaga ctggattttt 1500
gagacaatag aaagcattcc tcctccaaag gatcccgaga aattcctcgg tgacctctcc 1560
gaaaagttga aaatccgacg gatagagaga cgtatcgag aaatagatga tatgataaag 1620
aaagcttcaa acgatgaaga aaggcgtctt cttctctcta tgaaagtgga tctcctcaga 1680
aaaataaaga ggagg                                     1695

```

<210> 154

<211> 565

<212> PRT

<213> *Thermatoga maritima*

<400> 154

```

Met Ile Pro Arg Glu Val Ile Glu Glu Ile Lys Glu Lys Val Asp Ile
  1               5               10              15

```

```

Val Glu Val Ile Ser Glu Tyr Val Asn Leu Thr Arg Val Gly Ser Ser
      20               25              30

```

```

Tyr Arg Ala Leu Cys Pro Phe His Ser Glu Thr Asn Pro Ser Phe Tyr
    35               40              45

```

```

Val His Pro Gly Leu Lys Ile Tyr His Cys Phe Gly Cys Gly Ala Ser
    50               55              60

```

```

Gly Asp Val Ile Lys Phe Leu Gln Glu Met Glu Gly Ile Ser Phe Gln
    65               70              75              80

```

```

Glu Ala Leu Glu Arg Leu Ala Lys Arg Ala Gly Ile Asp Leu Ser Leu
      85               90              95

```

```

Tyr Arg Thr Glu Gly Thr Ser Glu Tyr Gly Lys Tyr Ile Arg Leu Tyr
    100              105             110

```

```

Glu Glu Thr Trp Lys Arg Tyr Val Lys Glu Leu Glu Lys Ser Lys Glu
    115              120             125

```

Ala Lys Asp Tyr Leu Lys Ser Arg Gly Phe Ser Glu Glu Asp Ile Ala
 130 135 140

Lys Phe Gly Phe Gly Tyr Val Pro Lys Arg Ser Ser Ile Ser Ile Glu
 145 150 155 160

Val Ala Glu Gly Met Asn Ile Thr Leu Glu Glu Leu Val Arg Tyr Gly
 165 170 175

Ile Ala Leu Lys Lys Gly Asp Arg Phe Val Asp Arg Phe Glu Gly Arg
 180 185 190

Ile Val Val Pro Ile Lys Asn Asp Ser Gly His Ile Val Ala Phe Gly
 195 200 205

Gly Arg Ala Leu Gly Asn Glu Glu Pro Lys Tyr Leu Asn Ser Pro Glu
 210 215 220

Thr Arg Tyr Phe Ser Lys Lys Lys Thr Leu Phe Leu Phe Asp Glu Ala
 225 230 235 240

Lys Lys Val Ala Lys Glu Val Gly Phe Phe Val Ile Thr Glu Gly Tyr
 245 250 255

Phe Asp Ala Leu Ala Phe Arg Lys Asp Gly Ile Pro Thr Ala Val Ala
 260 265 270

Val Leu Gly Ala Ser Leu Ser Arg Glu Ala Ile Leu Lys Leu Ser Ala
 275 280 285

Tyr Ser Lys Asn Val Ile Leu Cys Phe Asp Asn Asp Lys Ala Gly Phe
 290 295 300

Arg Ala Thr Leu Lys Ser Leu Glu Asp Leu Leu Asp Tyr Glu Phe Asn
 305 310 315 320

Val Leu Val Ala Thr Pro Ser Pro Tyr Lys Asp Pro Asp Glu Leu Phe
 325 330 335

Gln Lys Glu Gly Glu Gly Ser Leu Lys Lys Met Leu Lys Asn Ser Arg
 340 345 350

Ser Phe Glu Tyr Phe Leu Val Thr Ala Gly Glu Val Phe Phe Asp Arg
 355 360 365

Asn Ser Pro Ala Gly Val Arg Ser Tyr Leu Ser Phe Leu Lys Gly Trp
 370 375 380

Val Gln Lys Met Arg Arg Lys Gly Tyr Leu Lys His Ile Glu Asn Leu
 385 390 395 400

Val Asn Glu Val Ser Ser Ser Leu Gln Ile Pro Glu Asn Gln Ile Leu
 405 410 415

Asn Phe Phe Glu Ser Asp Arg Ser Asn Thr Met Pro Val His Glu Thr
 420 425 430

Lys Ser Ser Lys Val Tyr Asp Glu Gly Arg Gly Leu Ala Tyr Leu Phe
 435 440 445

Leu Asn Tyr Glu Asp Leu Arg Glu Lys Ile Leu Glu Leu Asp Leu Glu
 450 455 460

Val Leu Glu Asp Lys Asn Ala Arg Glu Phe Phe Lys Arg Val Ser Leu
 465 470 475 480

Gly Glu Asp Leu Asn Lys Val Ile Glu Asn Phe Pro Lys Glu Leu Lys
 485 490 495

Asp Trp Ile Phe Glu Thr Ile Glu Ser Ile Pro Pro Pro Lys Asp Pro
 500 505 510

Glu Lys Phe Leu Gly Asp Leu Ser Glu Lys Leu Lys Ile Arg Arg Ile
 515 520 525

Glu Arg Arg Ile Ala Glu Ile Asp Asp Met Ile Lys Lys Ala Ser Asn
 530 535 540

Asp Glu Glu Arg Arg Leu Leu Leu Ser Met Lys Val Asp Leu Leu Arg
 545 550 555 560

Lys Ile Lys Arg Arg
 565

<210> 155

<211> 804

<212> DNA

<213> Thermus thermophilus

<400> 155

atggctctac acccggtcca ccctggggca ataatcgggc acgaggccgt tctcgccctc 60
 cttccccgcc tcaccgcca gaccctgctc ttctccggcc ccgagggggt ggggcggcgc 120
 accgtggccc gctggtacgc ctgggggctc aaccgcggct tccccccgcc ctccctgggg 180
 gagcaccgcg acgtcctcga ggtggggccc aaggcccggg acctccggg ccgggccgag 240

```

gtgcggctgg aggaggtggc gccctcttg gagtggtgct ccagccacc cgggagcgg 300
gtgaaggtgg ccatcctgga ctcgccccac ctctcaccg aggcgcgcgc caacgccctc 360
ctcaagctcc tggaggagcc ccttctctac gcccgcatcg tcctcatcgc cccaagccgc 420
gccaccctcc tccccaccct ggcctcccgg gccacggagg tggcattcgc ccccggtgcc 480
gaggaggccc tgcgcgccct caccaggac ccggagctcc tccgctacgc cgcgggggcc 540
ccgggccgcc tccttagggc cctccaggac ccggaggggt accggggccc catggccagg 600
gcgcaaaggg tcctgaaagc cccgcccctg gagcgcctcg ctttgcttcg ggagcttttg 660
gccgaggagg aggggggtcca cgcctccac gccgtcctaa agcggccgga gcacctcctt 720
gccctggagc gggcgcgga ggcctggag ggtacgtga gcccgcgagc ggtcctcgcc 780
cgctggcct tagacttaga gaca
804

```

<210> 156

<211> 268

<212> PRT

<213> *Thermus thermophilus*

<400> 156

```

Met Ala Leu His Pro Ala His Pro Gly Ala Ile Ile Gly His Glu Ala
  1             5             10             15

```

```

Val Leu Ala Leu Leu Pro Arg Leu Thr Ala Gln Thr Leu Leu Phe Ser
          20             25             30

```

```

Gly Pro Glu Gly Val Gly Arg Arg Thr Val Ala Arg Trp Tyr Ala Trp
          35             40             45

```

```

Gly Leu Asn Arg Gly Phe Pro Pro Pro Ser Leu Gly Glu His Pro Asp
          50             55             60

```

```

Val Leu Glu Val Gly Pro Lys Ala Arg Asp Leu Arg Gly Arg Ala Glu
          65             70             75             80

```

```

Val Arg Leu Glu Glu Val Ala Pro Leu Leu Glu Trp Cys Ser Ser His
          85             90             95

```

```

Pro Arg Glu Arg Val Lys Val Ala Ile Leu Asp Ser Ala His Leu Leu
          100            105            110

```

```

Thr Glu Ala Ala Ala Asn Ala Leu Leu Lys Leu Leu Glu Glu Pro Pro
          115            120            125

```

```

Ser Tyr Ala Arg Ile Val Leu Ile Ala Pro Ser Arg Ala Thr Leu Leu
          130            135            140

```

```

Pro Thr Leu Ala Ser Arg Ala Thr Glu Val Ala Phe Ala Pro Val Pro
          145            150            155            160

```

Glu Glu Ala Leu Arg Ala Leu Thr Gln Asp Pro Glu Leu Leu Arg Tyr
 165 170 175
 Ala Ala Gly Ala Pro Gly Arg Leu Leu Arg Ala Leu Gln Asp Pro Glu
 180 185 190
 Gly Tyr Arg Ala Arg Met Ala Arg Ala Gln Arg Val Leu Lys Ala Pro
 195 200 205
 Pro Leu Glu Arg Leu Ala Leu Leu Arg Glu Leu Leu Ala Glu Glu Glu
 210 215 220
 Gly Val His Ala Leu His Ala Val Leu Lys Arg Pro Glu His Leu Leu
 225 230 235 240
 Ala Leu Glu Arg Ala Arg Glu Ala Leu Glu Gly Tyr Val Ser Pro Glu
 245 250 255
 Leu Val Leu Ala Arg Leu Ala Leu Asp Leu Glu Thr
 260 265

<210> 157
 <211> 729
 <212> DNA
 <213> Thermus thermophilus

<400> 157
 atgctggacc tgagggaggt gggggaggcg gaggggaagg ccctaaagcc ccttttggaa 60
 agcgtgcccg agggcgctcc cgtcctcctc ctggacccta agccaagccc ctcccgggcg 120
 gccttctacc ggaaccggga aaggcgggac ttccccaccc ccaaggggaa ggacctggtg 180
 cggcacctgg aaaaccgggc caagcgctg gggctcaggc tcccgggchg ggtggcccag 240
 tacctggcct cctggagggg ggacctcgag gccctggagc gggagctgga gaagcttgcc 300
 ctctctctcc caccctcac cctggagaag gtggagaagg tgggtggcct gaggcccccc 360
 ctcacgggct ttgacctggt gcgctccgtc ctggagaagg accccaagga ggccctcctg 420
 cgccataggc gcctcaagga ggagggggag gagccctca ggctcctcgg ggccctctcc 480
 tggcagttcg ccctcctcgc ccgggccttc ttctcctcc gggaaaaccc caggcccaag 540
 gaggaggacc tcgcccgcct cgaggcccac ccctacgccg ccgcccgcgc cctggaggcg 600
 gcgaagcgcc tcacggaaga ggccctcaag gaggccctgg acgcccctcat ggaggcgga 660
 aagagggccca agggggggaa agaccctgg ctcgcctgg aggcggcggt cctccgcctc 720
 gcccgttga 729

<210> 158
 <211> 292
 <212> PRT
 <213> Thermus thermophilus

<400> 158

Met Val Ile Ala Phe Thr Gly Asp Pro Phe Leu Ala Arg Glu Ala Leu
1 5 10 15

Leu Glu Glu Ala Arg Leu Arg Gly Leu Ser Arg Phe Thr Glu Pro Thr
20 25 30

Pro Glu Ala Leu Ala Gln Ala Leu Ala Pro Gly Leu Phe Gly Gly Gly
35 40 45

Gly Ala Met Leu Asp Leu Arg Glu Val Gly Glu Ala Glu Trp Lys Ala
50 55 60

Leu Lys Pro Leu Leu Glu Ser Val Pro Glu Gly Val Pro Val Leu Leu
65 70 75 80

Leu Asp Pro Lys Pro Ser Pro Ser Arg Ala Ala Phe Tyr Arg Asn Arg
85 90 95

Glu Arg Arg Asp Phe Pro Thr Pro Lys Gly Lys Asp Leu Val Arg His
100 105 110

Leu Glu Asn Arg Ala Lys Arg Leu Gly Leu Arg Leu Pro Gly Gly Val
115 120 125

Ala Gln Tyr Leu Ala Ser Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg
130 135 140

Glu Leu Glu Lys Leu Ala Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys
145 150 155 160

Val Glu Lys Val Val Ala Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu
165 170 175

Val Arg Ser Val Leu Glu Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu
180 185 190

Gly Gly Leu Lys Glu Glu Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala
195 200 205

Leu Ser Trp Gln Phe Ala Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg
210 215 220

Glu Asn Pro Arg Pro Lys Glu Glu Asp Leu Ala Arg Leu Glu Ala His
225 230 235 240

Pro Tyr Ala Ala Arg Arg Ala Leu Glu Ala Ala Lys Arg Leu Thr Glu
245 250 255

Glu Ala Leu Lys Glu Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg
260 265 270

Ala Lys Gly Gly Lys Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu
275 280 285

Arg Leu Ala Arg
290

<210> .159

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 159

gtgtgtcata tgagtaagga ttctgtccac cttcacc

37

<210> 160

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 160

gtgtgtggat ccgggggacta ctcggaagta aggg

34

<210> 161

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 161

gtgtgtcata tggaaaccac aatattccag ttccag

36

<210> 162

<211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 162
 gtgtgtggat ccttatccac catgagaagt atttttcac 39

 <210> 163
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 163
 gtgtgtcata tggaaaaagt tttttttgga aaaaactcca g 41

 <210> 164
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 164
 gtgtgtggat ccttaatccg cctgaacggc taacg 35

 <210> 165
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 165
 gtgtgtcata tgaactacgt tcccttcgcg agaaagtaca g 41

 <210> 166

<211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 166
 gtgtgtggat ccttaaaaca gcctcgtccc gctgga 36

 <210> 167
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 167
 gtgtgtcata tgcgcgttaa ggtggacagg gag 33

 <210> 168
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 168
 tgtgtctcga gtcattggcta caccctcatc ggcat 35

 <210> 169
 <211> 47
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 169
 gtgtgtcata tgctcaataa ggtttttata ataggaagac ttacggg 47

 <210> 170

<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 170
gtgtggatcc ttaaaaaggt atttcgtcct cttcatcgg 39

<210> 171
<211> 807
<212> DNA
<213> Thermus thermophilus

<400> 171
atggctcgag gcctgaaccg cgttttcctc atcggcgccc tcgccaccg gccggacatg 60
cgctacaccc cggcggggct cgccattttg gacctgacct tcgccgggtca ggacctgctt 120
ctttccgata acggggggga accggaggtg tcctgggtacc accgggtgag gctcttaggc 180
cgccaggcgg agatgtgggg cgacctcttg gaccaagggc agctcgtctt cgtggagggc 240
cgcttgaggt accgccagtg ggaaagggag ggggagaagc ggagcgagct ccagatccgg 300
gccgacttcc ggacccccctg gacgaccggg ggaagaagcg ggcggaggac agccggggcc 360
agcccaggct ccgcgccgcc ctgaaccagg tcttcctcat gggcaacctg acccgggacc 420
cggaactccg ctacaccccc cagggcaccg cgggtggccc gctgggcctg gcggtgaacg 480
agcgcgcgca gggggcgagg gagcgacccc acttcgtgga gggtcaggcc tggcgcgacc 540
tggcggagtg ggccgccgag ctgaggaagg gcgacggcct tttcgtgatc ggcaggttgg 600
tgaacgactc ctggaccagc tccagcggcg agcggcgctt ccagaccctg gtggaggccc 660
tcaggctgga gcgccccacc cgtggacctg cccaggcctg cccaggccgg cggaacaggt 720
cccgcgaagt ccagacgggt ggggtggaca ttgacgaagg cttggaagac tttccgccgg 780
aggaggattt gccgttttga gcacgaa 807

<210> 172
<211> 266
<212> PRT
<213> Thermus thermophilus

<400> 172
Met Ala Arg Gly Leu Asn Arg Val Phe Leu Ile Gly Ala Leu Ala Thr
1 5 10 15
Arg Pro Asp Met Arg Tyr Thr Pro Ala Gly Leu Ala Ile Leu Asp Leu
20 25 30
Thr Leu Ala Gly Gln Asp Leu Leu Leu Ser Asp Asn Gly Gly Glu Pro
35 40 45

Glu Val Ser Trp Tyr His Arg Val Arg Leu Leu Gly Arg Gln Ala Glu
 50 55 60
 Met Trp Gly Asp Leu Leu Asp Gln Gly Gln Leu Val Phe Val Glu Gly
 65 70 75 80
 Arg Leu Glu Tyr Arg Gln Trp Glu Arg Glu Gly Glu Lys Arg Ser Glu
 85 90 95
 Leu Gln Ile Arg Ala Asp Phe Leu Asp Pro Leu Asp Asp Arg Gly Lys
 100 105 110
 Lys Arg Ala Glu Asp Ser Arg Gly Gln Pro Arg Leu Arg Ala Ala Leu
 115 120 125
 Asn Gln Val Phe Leu Met Gly Asn Leu Thr Arg Asp Pro Glu Leu Arg
 130 135 140
 Tyr Thr Pro Gln Gly Thr Ala Val Ala Arg Leu Gly Leu Ala Val Asn
 145 150 155 160
 Glu Arg Arg Gln Gly Ala Glu Glu Arg Thr His Phe Val Glu Val Gln
 165 170 175
 Ala Trp Arg Asp Leu Ala Glu Trp Ala Ala Glu Leu Arg Lys Gly Asp
 180 185 190
 Gly Leu Phe Val Ile Gly Arg Leu Val Asn Asp Ser Trp Thr Ser Ser
 195 200 205
 Ser Gly Glu Arg Arg Phe Gln Thr Arg Val Glu Ala Leu Arg Leu Glu
 210 215 220
 Arg Pro Thr Arg Gly Pro Ala Gln Ala Cys Pro Gly Arg Arg Asn Arg
 225 230 235 240
 Ser Arg Glu Val Gln Thr Gly Gly Val Asp Ile Asp Glu Gly Leu Glu
 245 250 255
 Asp Phe Pro Pro Glu Glu Asp Leu Pro Phe
 260 265

<210> 173

<211> 992

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 173

```
aattccgaca tttcaattga atcgtttatt cgcgttgaaa aagaaggcaa gttgctcggt 60
gatgtgaaaa gaccggggag catcgtagct caggcgcgct ttttctctga aatcgtgaaa 120
aaactgccgc aacaaacggt ggaaatcgaa acggaagaca actttttgac gatcatccgc 180
tcggggcact cagaattccg cctcaatggg ctaaacgccg acgaatatcc gcgcctgccg 240
caaattgaag aagaaaacgt gtttcaaate ccggctgatt tattgaaaac cgtgattcgg 300
caaacggtgt tcgccgtttc tacatcggaac acgcgcccaa tcttgacagg tgtcaactgg 360
aaagttgaac atggcgagct tgtctgcaca gcgaccgaca gtcacgcgtt agccatgcgc 420
aaagtgaaaa ttgagtcgga aaatgaagta tcatacaacg tcgtcatccc tggaaaaagt 480
cttaatgagc tcagcaaaat tttggatgac ggcaaccacc cggtaggacat cgtcatgaca 540
gccaatcaag tgctatttaa ggccgagcac cttctcttct tttcccggtt gcttgacggc 600
aactatccgg agacggcccc cttgattcca acagaaagca aaacgaccat gatcgtcaat 660
gcaaaagagt ttctgcaggc aatcgaccga gcgtccttgc ttgctcgaga aggaaggaa 720
aacgttgtga aactgacgac gcttccttga ggaatgctcg aaatttcttc gatttctccg 780
agatcgggaa agtgacggag cagctgcaaa cggagtctct tgaaggggaa gagttgaaca 840
tttcgttcag cgcgaaatat atgatggacg cgttgccggc gcttgatgga acagacattt 900
caaatcagct tcaactgggc catgcggccg ttcctgttgc gcccgttca accgattcga 960
tgcttcagct cattttgccg gtgagaacat at 992
```

<210> 174

<211> 334

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 174

```
Asn Ser Asp Ile Ser Ile Ile Glu Ser Phe Ile Pro Leu Glu Lys Glu
 1             5             10             15

Gly Lys Leu Leu Val Asp Val Lys Arg Pro Gly Ser Ile Val Leu Gln
          20             25             30

Ala Arg Phe Phe Ser Glu Ile Val Lys Lys Leu Pro Gln Gln Thr Val
          35             40             45

Glu Ile Glu Thr Glu Asp Asn Phe Leu Thr Ile Ile Arg Ser Gly His
          50             55             60

Ser Glu Phe Arg Leu Asn Gly Leu Asn Ala Asp Glu Tyr Pro Arg Leu
          65             70             75             80

Pro Gln Ile Glu Glu Glu Asn Val Phe Gln Ile Pro Ala Asp Leu Leu
          85             90             95

Lys Thr Val Ile Arg Gln Thr Val Phe Ala Val Ser Thr Ser Glu Thr
          100            105            110

Arg Pro Ile Leu Thr Gly Val Asn Trp Lys Val Glu His Gly Glu Leu
```

115	120	125
Val Cys Thr Ala Thr Asp Ser His Arg Leu Ala Met Arg Lys Val Lys		
130	135	140
Ile Ile Glu Ser Glu Asn Glu Val Ser Tyr Asn Val Val Ile Pro Gly		
145	150	155
Lys Ser Leu Asn Glu Leu Ser Lys Ile Ile Leu Asp Asp Gly Asn His		
165	170	175
Pro Val Asp Ile Val Met Thr Ala Asn Gln Val Leu Phe Lys Ala Glu		
180	185	190
His Leu Leu Phe Phe Ser Arg Leu Leu Asp Gly Asn Tyr Pro Glu Thr		
195	200	205
Ala Arg Leu Ile Pro Thr Glu Ser Lys Thr Thr Met Ile Val Asn Ala		
210	215	220
Lys Glu Phe Leu Gln Ala Ile Asp Arg Ala Ser Leu Leu Ala Arg Glu		
225	230	235
Gly Arg Asn Asn Val Val Lys Leu Thr Thr Leu Pro Gly Gly Met Leu		
245	250	255
Glu Ile Ser Ser Ile Ser Pro Glu Ile Gly Lys Val Thr Glu Gln Leu		
260	265	270
Gln Thr Glu Ser Leu Glu Gly Glu Glu Leu Asn Ile Ser Phe Ser Ala		
275	280	285
Lys Tyr Met Met Asp Ala Leu Arg Ala Leu Asp Gly Thr Asp Ile Gln		
290	295	300
Ile Ser Phe Thr Gly Ala Met Arg Pro Phe Leu Leu Arg Pro Leu His		
305	310	315
Thr Asp Ser Met Leu Gln Leu Ile Leu Pro Val Arg Thr Tyr		
325	330	

<210> 175

<211> 492

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 175

```

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caatttcttg agccgaaagg aacgagcgag cagcgagggg cgacagcagg cggctactat 360
ggggatccat tcccattcgg gcaagatcag aaccaccaat atccgaacga aaaagggttt 420
ggccgcatcg atgacgatcc tttcgccaat gacggccagc cgatcgatat ttctgatgat 480
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```

<210> 176

<211> 164

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 176

```

Met Ile Asn Arg Val Ile Leu Val Gly Arg Leu Thr Arg Asp Pro Glu
  1             5             10             15

```

```

Leu Arg Tyr Thr Pro Ser Gly Val Ala Val Ala Thr Phe Thr Leu Ala
          20             25             30

```

```

Val Asn Arg Pro Phe Thr Asn Gln Ser Tyr Glu Asn Gln Glu Gly Arg
          35             40             45

```

```

Arg Val Tyr Val Thr Glu Val Val Ala Asp Ser Val Gln Phe Leu Glu
          50             55             60

```

```

Pro Lys Gly Thr Ser Glu Gln Arg Gly Ala Thr Ala Gly Gly Tyr Tyr
          65             70             75             80

```

```

Gln Gly Glu Arg Glu Thr Asp Phe Ile Gln Cys Val Val Trp Arg Arg
          85             90             95

```

```

Gln Ala Glu Asn Val Ala Asn Phe Leu Lys Lys Gly Ser Leu Ala Gly
          100            105            110

```

```

Val Asp Gly Arg Leu Gln Thr Arg Gly Asp Pro Phe Pro Phe Gly Gln
          115            120            125

```

```

Asp Gln Asn His Gln Tyr Pro Asn Glu Lys Gly Phe Gly Arg Ile Asp
          130            135            140

```

```

Asp Asp Pro Phe Ala Asn Asp Gly Gln Pro Ile Asp Ile Ser Asp Asp
          145            150            155            160

```

Asp Leu Pro Phe

<210> 177
 <211> 1044
 <212> DNA
 <213> *Bacillus stearothermophilus*

<400> 177
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 ggccccgagg agcgggagtg gaacttggct gtgtacgact gcgaggaaac gccgatcgag 180
 gcggcgcttg aggaggccga gacggtgccg ttttctggcg agcggcggtgt cattctcatc 240
 aagcatccat attttttttac gtctgaaaaa gagaaggaga tcgaacatga tttggcgaag 300
 ctggaggcgt acttgaaggc gccgtcgccg ttttcgatcg tcgtcttttt cgcgccgtac 360
 gagaagcttg atgagcgaaa aaaaattacg aagctcgcca aagagcaaag cgaagtcgtc 420
 atcgccgccc cgctcgccga agcggagctg cgtgcctggg tgcggcgccg catcgagagc 480
 caaggggccc aagcaagcga cgaggcgatt gatgtcctgt tgcggcgggc cgggacgcag 540
 ctttccgcct tggcgaatga aatcgataaa ttggccctgt ttgccggatc gggcggaacc 600
 atcgaggcgg cggcggttga gcggttgtc gccgcacgc cggaagaaaa cgtatttgtg 660
 cttgtcgagc aagtggcgaa gcgcgacatt ccagcagcgt tgcagacgtt ttatgatctg 720
 cttgaaaaca atgaagagcc gatcaaaatt ttggcggttg tcgccgccca tttccgcttg 780
 ctttcgcaag tgaaatggct tgcctcctta ggctacggac aggcgcaaat tgctgcggcg 840
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 ggagagcttg ctgaggcgat caacgagctc gctgacgccg attacgaagt gaaaagcggg 960
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 caagcggggc gccacggccg gcgg 1044

<210> 178
 <211> 348
 <212> PRT
 <213> *Bacillus stearothermophilus*

<400> 178
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 Leu Tyr Leu Leu Tyr Gly Asn Glu Pro Phe Leu Leu Thr Glu Thr Tyr
 20 25 30
 Glu Arg Leu Val Asn Ala Ala Leu Gly Pro Glu Glu Arg Glu Trp Asn
 35 40 45
 Leu Ala Val Tyr Asp Cys Glu Glu Thr Pro Ile Glu Ala Ala Leu Glu
 50 55 60
 Glu Ala Glu Thr Val Pro Phe Phe Gly Glu Arg Arg Val Ile Leu Ile

65		70		75		80									
Lys	His	Pro	Tyr	Phe	Phe	Thr	Ser	Glu	Lys	Glu	Lys	Glu	Ile	Glu	His
				85					90					95	
Asp	Leu	Ala	Lys	Leu	Glu	Ala	Tyr	Leu	Lys	Ala	Pro	Ser	Pro	Phe	Ser
			100					105					110		
Ile	Val	Val	Phe	Phe	Ala	Pro	Tyr	Glu	Lys	Leu	Asp	Glu	Arg	Lys	Lys
			115					120				125			
Ile	Thr	Lys	Leu	Ala	Lys	Glu	Gln	Ser	Glu	Val	Val	Ile	Ala	Ala	Pro
	130					135					140				
Leu	Ala	Glu	Ala	Glu	Leu	Arg	Ala	Trp	Val	Arg	Arg	Arg	Ile	Glu	Ser
145					150					155					160
Gln	Gly	Ala	Gln	Ala	Ser	Asp	Glu	Ala	Ile	Asp	Val	Leu	Leu	Arg	Arg
			165					170						175	
Ala	Gly	Thr	Gln	Leu	Ser	Ala	Leu	Ala	Asn	Glu	Ile	Asp	Lys	Leu	Ala
			180					185					190		
Leu	Phe	Ala	Gly	Ser	Gly	Gly	Thr	Ile	Glu	Ala	Ala	Ala	Val	Glu	Arg
	195						200					205			
Leu	Val	Ala	Arg	Thr	Pro	Glu	Glu	Asn	Val	Phe	Val	Leu	Val	Glu	Gln
	210					215					220				
Val	Ala	Lys	Arg	Asp	Ile	Pro	Ala	Ala	Leu	Gln	Thr	Phe	Tyr	Asp	Leu
225					230					235					240
Leu	Glu	Asn	Asn	Glu	Glu	Pro	Ile	Lys	Ile	Leu	Ala	Leu	Leu	Ala	Ala
			245					250						255	
His	Phe	Arg	Leu	Leu	Ser	Gln	Val	Lys	Trp	Leu	Ala	Ser	Leu	Gly	Tyr
			260					265					270		
Gly	Gln	Ala	Gln	Ile	Ala	Ala	Ala	Leu	Lys	Val	His	Pro	Phe	Arg	Val
	275						280					285			
Lys	Leu	Ala	Leu	Ala	Gln	Ala	Ala	Arg	Phe	Ala	Asp	Gly	Glu	Leu	Ala
	290					295					300				
Glu	Ala	Ile	Asn	Glu	Leu	Ala	Asp	Ala	Asp	Tyr	Glu	Val	Lys	Ser	Gly
305				310					315						320
Ala	Val	Asp	Arg	Arg	Leu	Ala	Val	Glu	Leu	Leu	Leu	Met	Arg	Trp	Gly

325

330

335

Ala Arg Pro Ala Gln Ala Gly Arg His Gly Arg Arg
340 345

<210> 179

<211> 757

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 179

```

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aaagcggcca gtttggtggt ggcgaaacgt ttgttttgtc tgtccccaat cggagtttcc 180
ccgtgtctag agtgccgcaa ctgccggcgc atcgactccg gcaaccaccc tgacgtccgg 240
gtgatcggcc cagatggagg atcaatcaaa aaggaacaaa tcgaatggct gcagcaagag 300
ttctcgaaaa cagcgtgtcga gtcggataaa aaaatgtaca tcgttgagca cgccgatcaa 360
atgacgacaa gcgctgccaa cagccttctg aaattttttg aagagccgca tccggggacg 420
gtggcgggat tgctgactga gcaataccac cgcctgctag ggacgatcgt ttcccgtgt 480
caagtgcctt cgttccggcc gttgccggcc gcagagctcg cccagggact tgtcgaggag 540
cacgtgccgt tgccgttggc gctggtggct gccatttga caaacagctt cgaggaagca 600
ctggcgcttg ccaaagatag ttggtttgcc gaggcgcgaa cattagtgt acaatggtat 660
gagatgctgg gcaagccgga gctgcagctt ttgtttttca tccacgaccg cttgtttccg 720
catttttttg aaagccatca gcttgacctt ggacttg 757

```

<210> 180

<211> 252

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 180

```

Met Arg Trp Glu Gln Leu Ala Lys Arg Gln Pro Val Val Ala Lys Met
  1             5             10             15

Leu Gln Ser Gly Leu Glu Lys Gly Arg Ile Ser His Ala Tyr Leu Phe
      20             25             30

Glu Gly Gln Arg Gly Thr Gly Lys Lys Ala Ala Ser Leu Leu Leu Ala
      35             40             45

Lys Arg Leu Phe Cys Leu Ser Pro Ile Gly Val Ser Pro Cys Leu Glu
      50             55             60

Cys Arg Asn Cys Arg Arg Ile Asp Ser Gly Asn His Pro Asp Val Arg
      65             70             75             80

```

Val Ile Gly Pro Asp Gly Gly Ser Ile Lys Lys Glu Gln Ile Glu Trp
85 90 95

Leu Gln Gln Glu Phe Ser Lys Thr Ala Val Glu Ser Asp Lys Lys Met
100 105 110

Tyr Ile Val Glu His Ala Asp Gln Met Thr Thr Ser Ala Ala Asn Ser
115 120 125

Leu Leu Lys Phe Leu Glu Glu Pro His Pro Gly Thr Val Ala Val Leu
130 135 140

Leu Thr Glu Gln Tyr His Arg Leu Leu Gly Thr Ile Val Ser Arg Cys
145 150 155 160

Gln Val Leu Ser Phe Arg Pro Leu Pro Pro Ala Glu Leu Ala Gln Gly
165 170 175

Leu Val Glu Glu His Val Pro Leu Pro Leu Ala Leu Leu Ala Ala His
180 185 190

Leu Thr Asn Ser Phe Glu Glu Ala Leu Ala Leu Ala Lys Asp Ser Trp
195 200 205

Phe Ala Glu Ala Arg Thr Leu Val Leu Gln Trp Tyr Glu Met Leu Gly
210 215 220

Lys Pro Glu Leu Gln Leu Leu Phe Phe Ile His Asp Arg Leu Phe Pro
225 230 235 240

His Phe Leu Glu Ser His Gln Leu Asp Leu Gly Leu
245 250

<210> 181

<211> 1677

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 181

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tacttatttt ccggcccgcg cggtacagga aaaacgagcg cagcgaaaat ttctgccaaag 180
gcggtcaact gtgaacaggc gccagcggcg gagccatgca atgagtgtcc agcttgcttc 240
ggcattacga atggaacggt tcccgatgtg ctggaaattg acgctgcttc caacaaccgc 300
gtcgatgaaa ttcgtgatat ccgtgagaag gtgaaatttg cgccaacgtc ggcccgtac 360
aaagtgtata tcatcgacga ggtgcatatg ctgtcgatcg gtgcgtttta cgcgctgttg 420
aaaacgttgagg agggccgcc gaaacacgtc attttcattt tggccacgac cgagccgcac 480


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aaaattccgg cgacgatcat ttcccgctgc caacgggttcg attttcgccg catcccgttt 540
caggcgatcg ttccacggct aaagtacgtc gcaagcgccc aaggtgtcga ggcgtcagat 600
gaggcattgt ccgccatcgc ccgtgctgca gacgggggga tgcgcgatgc gtcagcttg 660
cttgatcaag ccatttcgtt cagcgacggg aaacttcggc tcgacgacgt gctggcgatg 720
accggggctg catcatttgc cgccttatcg agcttcatcg aagccatcca ccgcaaagat 780
acagcggcgg ttcttcagca cttggaaacg atgatggcgc aagggaaaga tccgcatcgt 840
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gtggaggagg cgattcaaat tgctgtcgtt gacgaagcgt tcacttcact gtcggaaatg 960
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aaaataagag aagagttcat ccgcaataag gacgccatgg tggaaaaaag cgaagaagat 1620
ccgttaatcg ccgaagcgaa gcggctgttt ggcgaagagc tgatcgaaat taaagaa 1677

```

<210> 182

<211> 559

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 182

```

Val Ala Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Ala
  1                   5                   10                   15

```

```

Asp Met Val Gly Gln Glu His Val Thr Lys Thr Leu Gln Ser Ala Leu
          20                   25                   30

```

```

Leu Gln His Lys Ile Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
          35                   40                   45

```

```

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
          50                   55                   60

```

```

Glu Gln Ala Pro Ala Ala Glu Pro Cys Asn Glu Cys Pro Ala Cys Leu
          65                   70                   75                   80

```

```

Gly Ile Thr Asn Gly Thr Val Pro Asp Val Leu Glu Ile Asp Ala Ala
          85                   90                   95

```

```

Ser Asn Asn Arg Val Asp Glu Ile Arg Asp Ile Arg Glu Lys Val Lys
          100                  105                  110

```


Ala Ser Glu Leu Glu Pro Leu Ile Lys Arg Ile Glu Thr Leu Glu Ala
 370 375 380

Glu Leu Arg Arg Leu Lys Glu Gln Pro Pro Ala Pro Pro Ser Thr Ala
 385 390 395 400

Ala Pro Val Lys Lys Leu Ser Lys Pro Met Lys Thr Gly Gly Tyr Lys
 405 410 415

Ala Pro Val Gly Arg Ile Tyr Glu Leu Leu Lys Gln Ala Thr His Glu
 420 425 430

Asp Leu Ala Leu Val Lys Gly Cys Trp Ala Asp Val Leu Asp Thr Leu
 435 440 445

Lys Arg Gln His Lys Val Ser His Ala Ala Leu Leu Gln Glu Ser Glu
 450 455 460

Pro Val Ala Ala Ser Ala Ser Ala Phe Val Leu Lys Phe Lys Tyr Glu
 465 470 475 480

Ile His Cys Lys Met Ala Thr Asp Pro Thr Ser Ser Val Lys Glu Asn
 485 490 495

Val Glu Ala Ile Leu Phe Glu Leu Thr Asn Arg Arg Phe Glu Met Val
 500 505 510

Ala Ile Pro Glu Gly Glu Trp Gly Lys Ile Arg Glu Glu Phe Ile Arg
 515 520 525

Asn Lys Asp Ala Met Val Glu Lys Ser Glu Glu Asp Pro Leu Ile Ala
 530 535 540

Glu Ala Lys Arg Leu Phe Gly Glu Glu Leu Ile Glu Ile Lys Glu
 545 550 555

<210> 183

<211> 4301

<212> DNA

<213> Bacillus stearothermophilus

<400> 183

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 gaggagaaaa gctggcattt ttattttcag ttcgacaacg tgctgccggt tcatgtatac 180
 aaaacgtttg ccgatcggct gcagacggcg ttccgccata tcgccgccgt ccgccatacg 240

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cttgccgagc	tgcaagaagg	catgtcgccg	cttgtcgatt	ggctcagccg	gcagacgcct	360
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gagccggtgc	ggcggtttga	aacgatcgtc	gaagaagagc	ggcgctcgt	tgtgcaaggc	720
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 aattcgatc tgacggcaat tctctcattc cgccgttcaa cgccattccg gggcttgagg 4140
 cgaacgtggc gcaggcgatc gtgcgcgccc gcgaggaagg cgagtttttg tcgaaggagg 4200
 atttgcaaca gcgcggcaaa ttgtcgaaaa cgctgctcga gtatctagaa agccgcggct 4260
 gccttgactc gcttccagac cataaccagc tgctcgctgtt t 4301

<210> 184

<211> 1433

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 184

Met Val Thr Lys Glu Gln Lys Glu Arg Phe Leu Ile Leu Leu Glu Gln
 1 5 10 15

Leu Lys Met Thr Ser Asp Glu Trp Met Pro His Phe Arg Glu Ala Ala
 20 25 30

Ile Arg Lys Val Val Ile Asp Lys Glu Glu Lys Ser Trp His Phe Tyr
 35 40 45

Phe Gln Phe Asp Asn Val Leu Pro Val His Val Tyr Lys Thr Phe Ala
 50 55 60

Asp Arg Leu Gln Thr Ala Phe Arg His Ile Ala Ala Val Arg His Thr
 65 70 75 80

Met Glu Val Glu Ala Pro Arg Val Thr Glu Ala Asp Val Gln Ala Tyr
 85 90 95

Trp Pro Leu Cys Leu Ala Glu Leu Gln Glu Gly Met Ser Pro Leu Val
 100 105 110

Asp Trp Leu Ser Arg Gln Thr Pro Glu Leu Lys Gly Asn Lys Leu Leu
 115 120 125
 Val Val Ala Arg His Glu Ala Glu Ala Leu Ala Ile Lys Arg Arg Phe
 130 135 140
 Ala Lys Lys Ile Ala Asp Val Tyr Ala Ser Phe Gly Phe Pro Pro Leu
 145 150 155 160
 Gln Leu Asp Val Ser Val Glu Pro Ser Lys Gln Glu Met Glu Gln Phe
 165 170 175
 Leu Ala Gln Lys Gln Gln Glu Asp Glu Glu Arg Ala Leu Ala Val Leu
 180 185 190
 Thr Asp Leu Ala Arg Glu Glu Glu Lys Ala Ala Ser Ala Pro Pro Ser
 195 200 205
 Gly Pro Leu Val Ile Gly Tyr Pro Ile Arg Asp Glu Glu Pro Val Arg
 210 215 220
 Arg Leu Glu Thr Ile Val Glu Glu Glu Arg Arg Val Val Val Gln Gly
 225 230 235 240
 Tyr Val Phe Asp Ala Glu Val Ser Glu Leu Lys Ser Gly Arg Thr Leu
 245 250 255
 Leu Thr Met Lys Ile Thr Asp Tyr Thr Asn Ser Ile Leu Val Lys Met
 260 265 270
 Phe Ser Arg Asp Lys Glu Asp Ala Glu Leu Met Ser Gly Val Lys Lys
 275 280 285
 Gly Met Trp Val Lys Val Arg Gly Ser Val Gln Asn Asp Thr Phe Val
 290 295 300
 Arg Asp Leu Val Ile Ile Ala Asn Asp Leu Asn Glu Ile Ala Ala Asn
 305 310 315 320
 Glu Arg Gln Asp Thr Ala Pro Glu Gly Glu Lys Arg Val Glu Leu His
 325 330 335
 Leu His Thr Pro Met Ser Gln Met Asp Ala Val Thr Ser Val Thr Lys
 340 345 350
 Leu Ile Glu Gln Ala Lys Lys Trp Gly His Pro Ala Ile Ala Val Thr
 355 360 365

Asp	His	Ala	Val	Val	Gln	Ser	Phe	Pro	Glu	Ala	Tyr	Ser	Ala	Ala	Lys	370	375	380	
Lys	His	Gly	Met	Lys	Val	Ile	Tyr	Gly	Leu	Glu	Ala	Asn	Ile	Val	Asp	385	390	395	400
Asp	Gly	Val	Pro	Ile	Ala	Tyr	Asn	Glu	Thr	His	Arg	Arg	Leu	Ser	Glu	405	410	415	
Glu	Thr	Tyr	Val	Val	Phe	Asp	Val	Glu	Thr	Thr	Gly	Leu	Ser	Ala	Val	420	425	430	
Tyr	Asn	Thr	Ile	Ile	Glu	Leu	Ala	Ala	Val	Lys	Val	Lys	Asp	Gly	Glu	435	440	445	
Ile	Ile	Asp	Arg	Phe	Met	Ser	Phe	Ala	Asn	Pro	Gly	His	Pro	Leu	Ser	450	455	460	
Val	Thr	Thr	Met	Glu	Leu	Thr	Gly	Ile	Thr	Asp	Glu	Met	Val	Lys	Asp	465	470	475	480
Ala	Pro	Lys	Pro	Asp	Glu	Val	Leu	Ala	Arg	Phe	Val	Asp	Trp	Ala	Gly	485	490	495	
Asp	Ala	Thr	Leu	Val	Ala	His	Asn	Ala	Ser	Phe	Asp	Ile	Gly	Phe	Leu	500	505	510	
Asn	Ala	Gly	Leu	Ala	Arg	Met	Gly	Arg	Gly	Lys	Ile	Ala	Asn	Pro	Val	515	520	525	
Ile	Asp	Thr	Leu	Glu	Leu	Ala	Arg	Phe	Leu	Tyr	Pro	Asp	Leu	Lys	Asn	530	535	540	
His	Arg	Leu	Asn	Thr	Leu	Cys	Lys	Lys	Phe	Asp	Ile	Glu	Leu	Thr	Gln	545	550	555	560
His	His	Arg	Ala	Ile	Tyr	Asp	Ala	Glu	Ala	Thr	Gly	His	Leu	Leu	Met	565	570	575	
Arg	Leu	Leu	Lys	Glu	Ala	Glu	Glu	Arg	Gly	Ile	Leu	Phe	His	Asp	Glu	580	585	590	
Leu	Asn	Ser	Arg	Thr	His	Ser	Glu	Ala	Ser	Tyr	Arg	Leu	Ala	Arg	Pro	595	600	605	
Phe	His	Val	Thr	Leu	Leu	Ala	Gln	Asn	Glu	Thr	Gly	Leu	Lys	Asn	Leu	610	615	620	

Phe	Lys	Leu	Val	Ser	Leu	Ser	His	Ile	Gln	Tyr	Phe	His	Arg	Val	Pro	625	630	635	640
Arg	Ile	Pro	Arg	Ser	Val	Leu	Val	Lys	His	Arg	Asp	Gly	Leu	Leu	Val	645	650	655	
Gly	Ser	Gly	Cys	Asp	Lys	Gly	Glu	Leu	Phe	Asp	Asn	Leu	Ile	Gln	Lys	660	665	670	
Ala	Pro	Glu	Glu	Val	Glu	Asp	Ile	Ala	Arg	Phe	Tyr	Asp	Phe	Leu	Glu	675	680	685	
Val	His	Pro	Pro	Asp	Val	Tyr	Lys	Pro	Leu	Ile	Glu	Met	Asp	Tyr	Val	690	695	700	
Lys	Asp	Glu	Glu	Met	Ile	Lys	Asn	Ile	Ile	Arg	Ser	Ile	Val	Ala	Leu	705	710	715	720
Gly	Glu	Lys	Leu	Asp	Ile	Pro	Val	Val	Ala	Thr	Gly	Asn	Val	His	Tyr	725	730	735	
Leu	Asn	Pro	Glu	Asp	Lys	Ile	Tyr	Arg	Lys	Ile	Leu	Ile	His	Ser	Gln	740	745	750	
Gly	Gly	Ala	Asn	Pro	Leu	Asn	Arg	His	Glu	Leu	Pro	Asp	Val	Tyr	Phe	755	760	765	
Arg	Thr	Thr	Asn	Glu	Met	Leu	Asp	Cys	Phe	Ser	Phe	Leu	Gly	Pro	Glu	770	775	780	
Lys	Ala	Lys	Glu	Ile	Val	Val	Asp	Asn	Thr	Gln	Lys	Ile	Ala	Ser	Leu	785	790	795	800
Ile	Gly	Asp	Val	Lys	Pro	Ile	Lys	Asp	Glu	Leu	Tyr	Thr	Pro	Arg	Ile	805	810	815	
Glu	Gly	Ala	Asp	Glu	Glu	Ile	Arg	Glu	Met	Ser	Tyr	Arg	Arg	Ala	Lys	820	825	830	
Glu	Ile	Tyr	Gly	Asp	Pro	Leu	Pro	Lys	Leu	Val	Glu	Glu	Arg	Leu	Glu	835	840	845	
Lys	Glu	Leu	Lys	Ser	Ile	Ile	Gly	His	Gly	Phe	Ala	Val	Ile	Tyr	Leu	850	855	860	
Ile	Ser	His	Lys	Leu	Val	Lys	Lys	Ser	Leu	Asp	Asp	Gly	Tyr	Leu	Val	865	870	875	880

Gly	Ser	Arg	Gly	Ser	Val	Gly	Ser	Ser	Phe	Val	Ala	Thr	Met	Thr	Glu			
				885					890					895				
Ile	Thr	Glu	Val	Asn	Pro	Leu	Pro	Pro	His	Tyr	Val	Cys	Pro	Asn	Cys			
			900					905					910					
Lys	His	Ser	Glu	Phe	Phe	Asn	Asp	Gly	Ser	Val	Gly	Ser	Gly	Phe	Asp			
		915					920					925						
Leu	Pro	Asp	Lys	Asn	Cys	Pro	Arg	Cys	Gly	Thr	Lys	Tyr	Lys	Lys	Asp			
	930					935					940							
Gly	His	Asp	Ile	Pro	Phe	Glu	Thr	Phe	Leu	Gly	Phe	Lys	Gly	Asp	Lys			
945					950					955					960			
Val	Pro	Asp	Ile	Asp	Leu	Asn	Phe	Ser	Gly	Glu	Tyr	Gln	Pro	Arg	Ala			
				965					970					975				
His	Asn	Tyr	Thr	Lys	Val	Leu	Phe	Gly	Glu	Asp	Asn	Val	Tyr	Arg	Ala			
			980					985					990					
Gly	Thr	Ile	Gly	Thr	Val	Ala	Asp	Lys	Thr	Ala	Tyr	Gly	Phe	Val	Lys			
		995					1000					1005						
Ala	Tyr	Ala	Ser	Asp	His	Asn	Leu	Glu	Leu	Arg	Gly	Ala	Glu	Ile	Asp			
	1010					1015				1020								
Leu	Ala	Ala	Gly	Cys	Thr	Gly	Val	Lys	Arg	Thr	Thr	Gly	Gln	His	Pro			
1025					1030				1035					1040				
Gly	Gly	Ile	Ile	Val	Val	Pro	Asp	Tyr	Met	Glu	Ile	Tyr	Asp	Phe	Thr			
			1045					1050					1055					
Pro	Ile	Gln	Tyr	Pro	Ala	Asp	Asp	Thr	Ser	Ser	Glu	Trp	Arg	Thr	Thr			
		1060					1065						1070					
His	Phe	Asp	Phe	His	Ser	Ile	His	Asp	Asn	Leu	Leu	Lys	Leu	Asp	Ile			
		1075				1080						1085						
Leu	Gly	His	Asp	Asp	Pro	Thr	Val	Ile	Arg	Met	Leu	Gln	Asp	Leu	Ser			
	1090					1095				1100								
Gly	Ile	Asp	Pro	Lys	Thr	Ile	Pro	Thr	Asp	Asp	Pro	Asp	Val	Met	Gly			
1105					1110				1115					1120				
Ile	Phe	Ser	Ser	Thr	Glu	Pro	Leu	Gly	Val	Thr	Pro	Glu	Gln	Ile	Met			
			1125					1130					1135					

Cys Asn Val Gly Thr Ile Gly Ile Pro Glu Phe Gly Thr Arg Phe Val
 1140 1145 1150
 Arg Gln Met Leu Glu Glu Thr Arg Pro Lys Thr Phe Ser Glu Leu Val
 1155 1160 1165
 Gln Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Gly Asn Ala
 1170 1175 1180
 Gln Glu Leu Ile Gln Asn Gly Thr Cys Thr Leu Ser Glu Val Ile Gly
 1185 1190 1195 1200
 Cys Arg Asp Asp Ile Met Val Tyr Leu Ile Tyr Arg Gly Leu Glu Pro
 1205 1210 1215
 Ser Leu Ala Phe Lys Ile Met Glu Ser Val Arg Lys Gly Lys Gly Leu
 1220 1225 1230
 Thr Pro Glu Phe Glu Ala Glu Met Arg Lys His Asp Val Pro Glu Trp
 1235 1240 1245
 Tyr Ile Asp Ser Cys Lys Lys Ile Lys Tyr Met Phe Pro Lys Ala His
 1250 1255 1260
 Ala Ala Ala Tyr Val Leu Met Ala Val Arg Ile Ala Tyr Phe Lys Val
 1265 1270 1275 1280
 His His Pro Leu Leu Tyr Tyr Ala Ser Tyr Phe Thr Val Arg Ala Glu
 1285 1290 1295
 Asp Phe Asp Leu Asp Ala Met Ile Lys Gly Ser Pro Ala Ile Arg Lys
 1300 1305 1310
 Arg Ile Glu Glu Ile Asn Ala Lys Gly Ile Gln Ala Thr Ala Lys Glu
 1315 1320 1325
 Lys Ser Leu Leu Thr Val Leu Glu Val Ala Leu Glu Met Cys Glu Arg
 1330 1335 1340
 Gly Phe Ser Phe Lys Asn Ile Asp Leu Tyr Arg Ser Gln Ala Thr Glu
 1345 1350 1355 1360
 Phe Val Ile Asp Gly Asn Ser Leu Ile Pro Pro Phe Asn Ala Ile Pro
 1365 1370 1375
 Gly Leu Gly Thr Asn Val Ala Gln Ala Ile Val Arg Ala Arg Glu Glu
 1380 1385 1390

Gly Glu Phe Leu Ser Lys Glu Asp Leu Gln Gln Arg Gly Lys Leu Ser
1395 1400 1405

Lys Thr Leu Leu Glu Tyr Leu Glu Ser Arg Gly Cys Leu Asp Ser Leu
1410 1415 1420

Pro Asp His Asn Gln Leu Ser Leu Phe
1425 1430

<210> 185
<211> 199
<212> PRT
<213> Thermus thermophilus

<400> 185
Thr Pro Lys Gly Lys Asp Leu Val Arg His Leu Glu Asn Arg Ala Lys
1 5 10 15

Arg Leu Gly Leu Arg Leu Pro Gly Gly Val Ala Gln Tyr Leu Ala Ser
20 25 30

Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala
35 40 45

Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala
50 55 60

Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu
65 70 75 80

Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu Gly Arg Leu Lys Glu Glu
85 90 95

Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala
100 105 110

Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg Glu Met Pro Arg Pro Lys
115 120 125

Glu Glu Asp Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys
130 135 140

Ala Leu Leu Glu Ala Ala Arg Arg Leu Thr Glu Glu Ala Leu Lys Glu
145 150 155 160

Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg Ala Lys Gly Gly Lys

165

170

175

Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu Arg Leu Ala Arg Pro
 180 185 190

Ala Gly Gln Pro Arg Val Asp
 195

<210> 186

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 186

gcccagtagc tcgcctccct cgagggg

27

<210> 187

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 187

ggcccccttg gccttctcgg cctccat

27

<210> 188

<211> 331

<212> DNA

<213> Thermus thermophilus

<400> 188

agactcgagg ccctggagcg ggagctggag aagcttgccc tcctctcccc acccctcacc 60
 ctggagaagg tggagaaggt ggtggccctg aggcccccc tcacgggctt tgacctggtg 120
 cgctccgtcc tggagaagga cccaaggag gccctcctgc gcctcaggcg cctcaggag 180
 gagggggagg agcccctcag gctcctcggg gccctctcct ggcagttcgc cctcctcgcc 240
 cgggccttct tcctcctccg ggaaaacccc aggccaagg aggaggacct cgcccgccctc 300
 gagggcccacc cctacgccgc caagaaggcc a 331

<210> 189

<211> 110
<212> PRT
<213> Thermus thermophilus

<400> 189
Arg Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala Leu Leu Ser
1 5 10 15
Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala Leu Arg Pro
20 25 30
Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu Lys Asp Pro
35 40 45
Lys Glu Ala Leu Leu Arg Leu Arg Arg Leu Arg Glu Glu Gly Glu Glu
50 55 60
Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala Leu Leu Ala
65 70 75 80
Arg Ala Phe Phe Leu Leu Arg Glu Asn Pro Arg Pro Lys Glu Glu Asp
85 90 95
Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys Ala
100 105 110

<210> 190
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 190
gtggtgtcta gacatcataa cggttctggc a 31

<210> 191
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 191

gagggccacc accttctcca ctttctc 27

<210> 192

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 192

ctccgtcctg gagaaggacc ccaag 25

<210> 193

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<220>

<221> primer_bind

<222> (15)

<223> S at position 15 can be either C or G

<220>

<221> primer_bind

<222> (27)

<223> S at position 27 can be either C or G

<400> 193

cgcgaattca acgcsctcct caagacsct 29

<210> 194

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 194

gacacttaac atatggtcat cgccttcacc g 31

<210> 195
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 195
gtgtgtgaat tcgggtcaac gggcgaggcg gaggaccg

38

<210> 196
<211> 10
<212> PRT
<213> *Deinococcus radiodurans*

<400> 196
Val Ile Leu Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 197
<211> 10
<212> PRT
<213> *Methanococcus jannaschii*

<400> 197
Tyr Leu Ile Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 198
<211> 10
<212> PRT
<213> *Thermotoga maritima*

<400> 198
Leu Val Leu Asn Pro Gly Ser Ala Gly Arg
1 5 10

<210> 199
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 199

ctggtgaacc cgggctccgt gggccagc

28

<210> 200

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 200

Leu Leu Val Asn Pro Gly Ser Val Gly Gln

1

5

10

<210> 201

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 201

ctcgaggagc ttgaggaggg tggtggc

27

<210> 202

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 202

Ala Asn Thr Leu Leu Lys Leu Leu Glu

1

5

<210> 203

<211> 32

<212> PRT

<213> *Deinococcus radiodurans*

<400> 203

Gly Phe Gly Gly Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Leu Ser Pro Arg His Asn Val Arg Glu Asp Glu Tyr Gly Gly
20 25 30

<210> 204

<211> 32

<212> PRT

<213> *Caenorhabditis elegans*

<400> 204

Gly Phe Asp Gly Ile Gln Leu His Gly Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Thr Ser Pro Thr Thr Asn Lys Arg Val Asp Lys Tyr Gly Gly
20 25 30

<210> 205

<211> 32

<212> PRT

<213> *Pseudomonas aeruginosa*

<400> 205

Gly Phe Ser Gly Val Glu Ile His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Leu Ser Pro Leu Ser Asn Arg Arg Ser Asp Ala Trp Gly Gly
20 25 30

<210> 206

<211> 32

<212> PRT

<213> Archaeoglobus fulgidus

<400> 206

Gly Phe Asp Ala Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Glu Phe Ile Ser Pro His Val Asn Arg Arg Lys Asp Glu Tyr Gly Gly
20 25 30

<210> 207

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 207

catcctggac tcggcccacc tcctcaccga 30

<210> 208

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 208

Ile Leu Asp Ser Ala His Leu Leu Thr
1 5

<210> 209

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 209

gaggaggtag ccgtgggccg cgtggagctc cac 33

<210> 210
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 210
Val Glu Leu His Ala Ala His Gly Tyr Leu Leu
1 5 10

<210> 211
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 211
ggctttccca tatggctcta caccggtc ac 32

<210> 212
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 212
gcgtgatcc acggtcatgt ctctaagtc 29